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OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 18:37:58 ; Search time 3870.2 Seconds  
(without alignments)  
11838.012 Million cell updates/sec

Title: US-09-378-759-10  
Perfect score: 2962  
Sequence: 1 CTCGTCGCCCGCGTGAAGA.....CCAGCCCCGCCCTCTGC 2962

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
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3: gb\_ba3:\*  
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8: gb\_ov:\*  
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93: gb\_v46:\*  
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96: gb\_v49:\*  
97: gb\_v50:\*  
98: em\_ba3:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2962	100.0	2962	9 AR084949	AR084949 Sequence
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4	2233	75.4	3949	9 AX034855	AX034855 Sequence
5	2233	75.4	3949	88 AF025304	AF025304 Homo sapl
6	1996	67.4	3768	9 AX034853	AX034853 Sequence
7	1996	67.4	3768	97 HUMDRK	L41939 Homo sapien
8	1673	56.5	3151	97 HUMERKA	D31661 Human mRNA

9	1015	34.3	1618	97	HUMERK1P	D37827 Homo sapien
10	692	23.4	1225	97	HUMERK	D14717 Human mRNA
C 11	637	21.5	181529	81	AL512444	AL512444 Homo sapi
C 12	586	19.8	171553	63	AC013611	AC013611 Homo sapi
C 13	251	8.5	111026	79	AL157403	AL157403 Homo sapi
C 14	251	8.5	113956	92	HS74M1	AL035704 Human DNA
C 15	251	8.5	149709	73	AC067727	AC067727 Homo sapi
C 16	183	6.2	189	93	HSERKD23	X59292 Human erk g
C 17	120	4.1	171	45	E09453	E09453 CDNA encodl
C 18	59	2.0	3921	97	HUMERK	M59371 Human prote
C 19	59	2.0	157132	81	AL451042	AL451042 Homo sapi
C 20	59	2.0	160242	69	AC025928	AC025928 Homo sapi
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22	49	1.7	1153	8	AB025542	AB025542 Lampetra
23	48	1.6	3104	94	MUSNRK	L25890 Mus musculu
24	47	1.6	1635	94	MUSNRK	X76011 M.musculu
25	41	1.4	3873	94	MMU07634	MMU07634 Mus muscu
26	36	1.3	2664	8	AF026039	AF026039 Xenopus 1
27	36	1.2	175	94	MMMPK5	X57243 M.musculu
28	35	1.2	162	9	AR062730	AR062730 Sequence
29	35	1.2	3733	94	MMU06834	U06834 Mus musculu
30	35	1.2	4479	94	MMU06834	Z49085 M.musculu
31	35	1.2	296820	94	AF312033	AF312033 Mus muscu
32	32	1.1	1294	94	MMECK2	X76010 M.musculu
33	32	1.1	3395	94	MMECK	X76010 M.musculu
34	32	1.1	3712	8	GGU23783	U23783 Gallus gall
35	32	1.1	3776	10	IL15003	IL15003 Sequence 7
36	32	1.1	286552	76	AC079559	AC079559 Mus muscu
37	30	1.0	2839	88	AF037333	X75208 H.sapiens H
38	29	1.0	3060	8	CCOER3PRT	X91737 C.cotturix
39	29	1.0	3133	10	IL15000	IL15000 Sequence 1
40	29	1.0	3135	8	GGCEK6A	Z19110 G.gallus Ce
41	29	1.0	3227	8	CHCEK5	M62325 Chicken emb
42	29	1.0	3592	9	AR062743	AR062743 Sequence
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44	29	1.0	3871	97	HUMERK1P2R	L40636 Homo sapien
45	29	1.0	3871	97	HUMERK1P2R	L40636 Homo sapien

## ALIGNMENTS

**RESULT 1**  
**LOCUS** AR084933  
**DEFINITION** Sequence 10 from patent US 5981245.  
**ACCESSION** AR084933  
**VERSION** AR084933.1  
**KEYWORDS** GI:10011704  
**SOURCE** Unknown.  
**ORGANISM** Unclassified.  
**REFERENCE** 1 (bases 1 to 2962)  
**AUTHORS** Fox, G.M., Welcher, A.A. and Jing, S.  
**TITLE** Eph-like receptor protein tyrosine kinases  
**JOURNAL** Patent: US 5981245-A 10 09-NOV-1999;  
**FEATURES** Location/Qualifiers  
**source** 1..2962  
**BASE COUNT** 654 a 914 c 827 g 567 t  
**ORIGIN**

**Query Match** 100.0%; Score 2962; DB 9; Length 2962;  
**Best Local Similarity** 100.0%; Pred. No. 0;  
**Matches 2962; Conservative** 0; Mismatches 0; Indels 0; Gaps 0;

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**DB** 1 TGGATGTCATCTCTCTCCATCAGAGGTGGGAAGAGTGTAGTACATGAGAAATGAAC 120

**DB** 61 TGGATGTCATCTCTCCATCAGAGGTGGGAAGAGTGTAGTACATGAGAAATGAAC 120  
**QY** 121 ACGATCCGACGTAACAGGTGTGCAACGTTTGTAGTCAAGCCAGAACTGGCTACGG 180  
**DB** 121 ACGATCCGACGTAACAGGTGTGCAACGTTTGTAGTCAAGCCAGAACTGGCTACGG 180  
**QY** 181 ACCAGTTTATCCGGGCGCCGGGGCCCGCCAGCATCCACGTGGAGATGAAGTTTGGTG 240  
**DB** 181 ACCAGTTTATCCGGGCGCCGGGGCCCGCCAGCATCCACGTGGAGATGAAGTTTGGTG 240  
**QY** 241 CGTACTGACAGCAGATCCCGAGCGTGTGCTGCTGCTGCAAGAGAGACCTTCAACCTTAT 300  
**DB** 241 CGTACTGACAGCAGATCCCGAGCGTGTGCTGCTGCTGCAAGAGAGACCTTCAACCTTAT 300  
**QY** 301 TACTATAGGCTGACTTTGACTGCGCCACCAAGACCTTCCCAACTGATGAGAAATCCA 360  
**DB** 301 TACTATAGGCTGACTTTGACTGCGCCACCAAGACCTTCCCAACTGATGAGAAATCCA 360  
**QY** 361 TGGGTGAAGGGAATACCATTTGACCGCAGAGAGATTTCCAGAGAGACCTTCAACCTTAT 420  
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**QY** 721 ATGTGCAAGGAGGCTTTCGAGGCGGTTGAGAAATGAGACCGTGTCCGAGGTTGTCAAT 780  
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 VERSION AR084949.1  
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 ORGANISM  
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 UNCLASSIFIED.  
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 AUTHORS Fox,G.M., Weicher,A.A. and Jing,S.  
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[illegible]

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ORIGIN			
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Best Local Similarity	100.0%	Pred. No. 0:	
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ACCESSION AX034855 GI:11190806  
VERSION AX034855.1  
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AUTHORS Vinals, I.D.  
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JOURNAL Patent: WO 0053216-A 3 14-SEP-2000;  
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 REFERENCE  
 1 (bases 1 to 3949)  
 Ikegaki,N., Tang,X.X., Liu,X.G., Biegel,J.A., Allen,C.,  
 Yoshida,A., Sulman,E.P., Brodeur,G.M. and Pleasure,D.E.  
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 (EPH2): a developmentally regulated human protein-tyrosine kinase  
 gene of the FPH family  
 Hum. Mol. Genet. 4 (11), 2033-2045 (1995)  
 JOURNAL  
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 96154673  
 2 (bases 1 to 3949)  
 Tang,X.X., Pleasure,D.E., Brodeur,G.M. and Ikegaki,N.  
 A variant transcript encoding an isoform of the human protein  
 tyrosine kinase EPHB2 is generated by alternative splicing and  
 alternative use of polyadenylation signals  
 Oncogene 17 (4), 521-526 (1998)  
 JOURNAL  
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 3 (bases 1 to 3949)  
 Ikegaki,N. and Tang,X.X.  
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 Submitted (15-SEP-1997) Oncology, The Children's Hospital of  
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BASE COUNT  
ORIGIN

934 a 1142 c 1105 g 768 t

Query Match	Similarity	99.6%	Pred. No. 0:	Matches 2903:	Conservative	0:	Mismatches	5:	Indels	6:	Gaps
Qy	1	CTCTCGCCGCGGTGGAGMAACGCTAATGAGACTCCACTACGCGACTGCTGAGCTGGC	60								
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Qy	61	TGAGTGGTGATTCCTCCATCAGGGTGGGAAGGGTGAAGTGGCTACGATGGAACATGAAC	120								
Db	128	TGAGTGGTGATTCCTCCATCAGGGTGGGAAGGGTGAAGTGGCTACGATGGAACATGAAC	187								
Qy	121	ACGATCCGACGACGACGAGGTGTGCAACGTTTGAGTCAACCCAGAACACTGGCTACGG	180								
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Qy	181	ACCAAGTTTATTCGGGCGCGTGGGGCCCAACGCGATCCACGTGGAGATGAAGTTTGGGTG	240								
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Qy	241	CGTGACTGCAAGCATGCCCAAGCGGCTGGGCTGCTCAAGGAGACCTTAACTCTAT	300								
Db	308	CGTGACTGCAAGCATGCCCAAGCGGCTGGGCTGCTCAAGGAGACCTTAACTCTAT	367								
Qy	301	TACTATGAGCTACATTTGACTGGGCAACAGACCTTCCCACTGGATGGAATCA	360								
Db	368	TACTATGAGCTACATTTGACTGGGCAACAGACCTTCCCACTGGATGGAATCA	427								
Qy	361	TGGGTGAAGGTGATACATTTGCAAGCCGACGAGAGCTTCTCCAGTGGACCTGGGTGC	420								
Db	428	TGGGTGAAGGTGATACATTTGCAAGCCGACGAGAGCTTCTCCAGTGGACCTGGGTGC	487								
Qy	421	CGCGTCATGAAATCAACACCGAGGTGGGAGCTTGGGACCTGTTCGCGAGCGGCTTC	480								
Db	488	CGCGTCATGAAATCAACACCGAGGTGGGAGCTTGGGACCTGTTCGCGAGCGGCTTC	547								
Qy	481	TACCTGGGCTTCCAGGACATATGGCGGCTGCATGTCCCTCATGCGCGTGTCTTTAC	540								
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Qy	541	CGCAAGTCCCCGCGATCCAGAAATGGCGCCATTTCCAGGAAACCCTGTGCGGGGCT	600								

Db	608	CGCAGATGCCCCCGCATTCACGAAATGGCCCATCTTCCAGSAAACCCGTGCGGGGCT	667
Qy	601	GAGAGCAGATCGTGGTGGCTGCCGGGGCAGCTGCATCGCCAAATGCGAAGAGTGGAT	660
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Db	848	GGGACTTCAAGGCCCAACCAAGGGATAGAGCTGTACCACATGTCCATCAACACCGG	907
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 LOCUS AX034853  
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 ACCESSION AX034853  
 VERSION AX034853.1 GI:11190805  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3768)  
 AUTHORS Vinals, Y.D.  
 TITLE Novel uses  
 JOURNAL Patent: WO 0053216-A 1 14-SEP-2000;  
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 Matches 2956; Conservative 0; Mismatches 6; Indels 9; Gaps 2;  
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DEFINITION Homo sapiens (clone FBK III 11c) protein-tyrosine kinase (DRT)  
ACCESSION L41939.1 GI:1100109  
VERSION DRT gene; EPH gene family; protein-tyrosine kinase.  
KEYWORDS Homo sapiens (clone: FBK III 11c) (clone library: Stratagene,  
SOURCE Zapit, 936026) midterm fetus brain cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 3768)  
AUTHORS Ikegaki,N., Tang,X.X., Biegel,J.A., Allen,C.,  
Yoshioka,A., Sulman,E.P., Brodeur,G.M. and Pleasure,D.E.  
TITLE Molecular characterization and chromosomal localization of DRT  
(EPH3): a developmentally regulated human protein-tyrosine kinase  
JOURNAL Hum. Mol. Genet. 4 (11), 2033-2045 (1995)  
MEDLINE 96154673  
FEATURES  
source location/Qualifiers  
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DEFINITION Homo sapiens mRNA for large erk/cek5 tyrosine kinase, partial cds.  
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VERSION D37827.1 GI:1060894  
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ORGANISM Homo sapiens  
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Saito, T.  
Direct Submission  
Submitted (01-AUG-1994) to the DDBJ/EMBL/GenBank databases.  
Toshiyuki Saito, National Institute of Radiological Sciences; 9-1  
Anagawa 4-chome, Inage-ku, Chiba 263, Japan  
(Tel:043-251-2111(ex.361), Fax:043-256-8301)  
2 (sites)  
Chap, J. and Watt, V.M.  
erk and erk, new members of the eph subclass of receptor  
protein-tyrosine kinases  
Oncogene 6 (6), 1057-1061 (1991)  
91296384  
3 (sites)  
Iwase, T., Tanaka, M., Suzuki, M., Naito, Y., Sugimura, H. and Kino, I.  
Identification of protein-tyrosine kinase genes preferentially  
expressed in embryo stomach and gastric cancer  
Biochem. Biophys. Res. Commun. 194 (2), 698-705 (1993)  
93343925  
4 (bases 1 to 1618)  
Saito, T., Naohiko, S., Kitahara, M., Murata, M., Yamamoto, Y., Horii, T.  
and Matsuda, Y.  
Identification of human erk gene as a putative receptor tyrosine  
kinase and its chromosomal localization to 1p36.1: a comparative  
mapping of human, mouse and rat chromosomes  
Unpublished (1994)  
On Nov 13, 1995 this sequence version replaced gi:529066.  
Submitted (01-AUG-1994) to DDBJ by:  
Toshiyuki Saito  
National Institute of Radiological Sciences  
Division of Genetics  
9-1 Anagawa 4-chome, Inage-ku  
Chiba 263  
Japan  
Phone: 043-251-2111 x333  
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Db 13 GTGCGAGGCTACGCGGCGCTACGCGGCAAGATGTACTTCAGACCAATGACAGAGCGAG 72  
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Db 253 ATGAAGATCTACATCGATCCTTTACCTACGAGAGACCCCAAGAGGAGTGGCGAGTTT 312  
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OY 2089 CAAAAGAGTGGGCAATTCACATCATCCAGCTGTGTGGGAGTCTTGGGGAGTATCCAGCT 2148  
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Db	913	GGCATTGTGATGGAGAGTGTGCTTATGAGGAGCGGCGCTACTGGGACATGACCAAC	972
QY	2449	CAGGATGTATCAATGCCATTGAGAGAGATGCGGCTGGCCAGCATGAGACTGCCCCG	2508
Db	973	CAGGATGTATCAATGCCATTGAGAGAGATGCGGCTGGCCAGCATGAGACTGCCCCG	1032
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QY	2809	ATTCTCGGGTGGGGGCTTGGCTGGGCGACAGAAAAAATCCTGAACAGTATCCAG	2868
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RESULT 10  
LOCUS HUMERK 1225 bp mRNA PRI 23-JUN-1999  
DEFINITION Human mRNA for large erk kinase.  
ACCESSION D14717.1 GI:285916  
VERSION D14717.1  
KEYWORDS large erk kinase.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Chan, J. and Watt, V.M.  
TITLE erk and erk, new members of the eph subclass of receptor protein-tyrosine kinases  
JOURNAL Oncogene 6 (6), 1057-1061 (1991)

MEDLINE	91296384																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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Db 336 CATCTCGTCAACAGCAACCTGTGTCGAAGGTGTGCACTTTGGGCTCTACGCTTTCT 395
QY 2265 AGAGAGCATACCTCAGACCCCACTTACACACAGTGCCTGGGGCGAAGTTCCTCCATCG 2324
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QY 2325 CTGGACAGCCCCGGGAAGCCATCCTACCTACCGAAGTTCACTTCGGCCAGTGTGTGAG 2384
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RESULT 11
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LOCUS Homo sapiens chromosome 1 clone RP11-69E9, *** SEQUENCING IN
DEFINITION PROGRESS ***, 8 unordered pieces.
ACCESSION AL512444
VERSION AL512444.6 GI:12192913
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 181529)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 13, 2001 this sequence version replaced gi:12044686.
COMMENT

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----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA69E9
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 17625 bases at least Q40
Consensus quality: 179440 bases at least Q30
Consensus quality: 180200 bases at least Q20
Insert size: 180829; sum-of-contris
Insert size: 174363; 7.5% error; agarose-fp
Quality coverage: 6.77x in Q20 bases; sum-of-contris Quality
coverage: 7.07x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 12367: contig of 12367 bp in length
12368 12467: gap of 100 bp
12468 20480: contig of 8013 bp in length
20481 20580: gap of 100 bp
20581 23242: contig of 2662 bp in length
23243 23342: gap of 100 bp
23343 88023: contig of 64681 bp in length
88024 83123: gap of 100 bp
88124 102351: contig of 14228 bp in length
102352 102451: gap of 100 bp
102452 117171: contig of 14720 bp in length
117172 117271: gap of 100 bp
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BASE COUNT 42344 a 47438 c 46236 g 44808 t 703 others  
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Query Match 21.5%; Score 637; DB 81; Length 181529;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 687; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Y 144 CAACGTGTGTGAGTCAAGCAAGCAACTGGCTACGACCAAGTTATCCGCGCCGTG 203  
 DB 39718 CAACGTGTGTGAGTCAAGCAAGCAACTGGCTACGACCAAGTTATCCGCGCCGTG 39659  
 Y 204 GGGCCACCGCATCCACGTGAGATGAAGTTTGGTGGTGGTGGTGGTGGTGGTGG 263  
 DB 39658 GGGCCACCGCATCCACGTGAGATGAAGTTTGGTGGTGGTGGTGGTGGTGGTGG 39599  
 Y 264 CGTGGCTGGCTGGCTGGCAAGGAGACCTTCAACCTGATGAGGCTGACTTGGATC 323  
 DB 39598 CGTGGCTGGCTGGCTGGCAAGGAGACCTTCAACCTGATGAGGCTGACTTGGATC 39539  
 Y 324 GGGCACCAGACCTTCCCAACTGGATGAGATGATCCATGAGGTGAGGTGATGATG 383  
 DB 39538 GGGCACCAGACCTTCCCAACTGGATGAGATGATCCATGAGGTGAGGTGATGATG 39479  
 Y 384 AGCCGACGAGAGCTTCTCCAGGTGGAGCTGGTGGCGGCTCATGAAATCAACACCG 443  
 DB 39478 AGCCGACGAGAGCTTCTCCAGGTGGAGCTGGTGGCGGCTCATGAAATCAACACCG 39419  
 Y 444 GGTGGGAGCTTTCGAGCTGTGTCGCCGAGGCGCTTACCTGGCTTCCAGACTATG 503  
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 Y 564 CAATGGCCCATCTTCCAGAGAAACCTGTCGGGGCTAGAGCAACATGGCTGGTGGCTG 623  
 DB 39298 CAATGGCCCATCTTCCAGAGAAACCTGTCGGGGCTAGAGCAACATGGCTGGTGGCTG 39239  
 Y 624 CGGGGCAAGTGCATCGCAATCGGAGAGGTGATGATCCATCAAGCTTACTGTAA 683  
 DB 39238 CGGGGCAAGTGCATCGCAATCGGAGAGGTGATGATCCATCAAGCTTACTGTAA 39179  
 Y 684 CGGGGCAAGTGCATCGGCTGCTGCCATCGGGCGCTGATGCAAGCAAGGCTTGAAGC 743  
 DB 39178 CGGGGCAAGTGCATCGGCTGCTGCCATCGGGCGCTGATGCAAGCAAGGCTTGAAGC 39119  
 Y 744 CGTTGAGATGCGACCGTCTGCCGAGT 771  
 DB 39118 CGTTGAGATGCGACCGTCTGCCGAGT 39091

RESULT 12  
 AC013611/c AC013611 171553 bp DNA HTG 30-MAR-2000  
 LOCUS Homo sapiens clone RP11-10K8, WORKING DRAFT SEQUENCE, 11 unordered  
 DEFINITION pieces.  
 AC013611.3 GI:7341870  
 VERSION  
 KEYWORDS  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 171553)  
 AUTHORS  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 TITLE  
 JOURNAL  
 COMMENT  
 2 (bases 1 to 171553)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collumore, A.,  
 Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
 Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
 Galagan, J., Gardy, S., Grant, G., Hays, B., Heaford, A., Horon, L.,  
 Howland, J., Johnson, R., Jones, C., Kann, L., Karates, A., Klein, J.,  
 Lehoczy, J., Liu, C., Locke, K., MacDonald, P., Margulis, N.,  
 McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Melidrim, J.,  
 Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,  
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Testa, S., Tjelle, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
 Wyman, D., Ye, W., J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 30, 2000 this sequence version replaced g1:6532099.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RW/RepeatMasker.html  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR  
 Web site: http://www.seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L3093  
 Center clone name: 10\_K\_8  
 Summary Statistics  
 Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 165779 bases at least Q40  
 Consensus quality: 168407 bases at least Q30  
 Consensus quality: 169490 bases at least Q20  
 Insert size: 16900; agarose-fp  
 Insert size: 17053; sum-of-ctnigs  
 Quality coverage: 5.5 in Q20 bases; agarose-fp  
 Quality coverage: 5.4 in Q20 bases; sum-of-ctnigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 11 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 2990: contig of 2990 bp in length  
 2991 3090: gap of 100 bp  
 3091 7743: contig of 4653 bp in length  
 7744 7843: gap of 100 bp  
 7844 12243: contig of 4400 bp in length  
 12244 12343: gap of 100 bp  
 12344 17166: contig of 4823 bp in length  
 17167 17266: gap of 100 bp  
 17267 24222: contig of 6956 bp in length  
 24223 24323: gap of 100 bp  
 24323 33192: contig of 8870 bp in length  
 33193 33292: gap of 100 bp  
 33293 51470: contig of 18178 bp in length  
 51471 51570: gap of 100 bp  
 51571 72899: contig of 21329 bp in length  
 72900 72999: gap of 100 bp  
 73000 91876: contig of 18877 bp in length  
 91877 91976: gap of 100 bp  
 91977 128638: contig of 36662 bp in length  
 128639 128738: gap of 100 bp  
 128739 171553: contig of 42815 bp in length.

Location/Qualifiers  
 1. 171553

FEATURES  
 source



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  7844..12243
misc_feature
  /note="assembly_fragment"
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  24323..33192
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  clone_end:T7
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  91977..128638
misc_feature
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  128739..171553
misc_feature
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BASE COUNT 41218 a 43858 c 43894 g 41573 t 1010 others
ORIGIN

```

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 84 GTGGGAAGAGGTGATGCGTACATGAGAACATGACACGATCCGACGTACAGGTGTG 143
    |||||||
Db 145073 GTGGGAAGAGGTGATGCGTACATGAGAACATGACACGATCCGACGTACAGGTGTG 145014

QY 144 CAACGTGTGTGAGCAAGCCAGAACAACTGGCTACGACCAAGTTATCCGGCCGTGG 203
    |||||||
Db 145013 CAACGTGTGTGAGCAAGCCAGAACAACTGGCTACGACCAAGTTATCCGGCCGTGG 144954

QY 204 GGCCCAACCCGATCCACGTGAGATGAAGTTTGGTGGCTGACTGACGACATCCCGAG 263
    |||||||
Db 144953 GGCCCAACCCGATCCACGTGAGATGAAGTTTGGTGGCTGACTGACGACATCCCGAG 144894

QY 264 CGTGCTGGCTCTCGAAGAGACCTTCAACCTCTATTACTATGAGGCTGACTTGTACTC 323
    |||||||
Db 144893 CGTGCTGGCTCTCGAAGAGACCTTCAACCTCTATTACTATGAGGCTGACTTGTACTC 144834

QY 324 GGCCCAACGATCCCACTGATGAGATGGAATCCATGGGTGAAGTGGATTCATTCG 383
    |||||||
Db 144833 GGCCCAACGATCCCACTGATGAGATGGAATCCATGGGTGAAGTGGATTCATTCG 144774

QY 384 AGCCGACGAGAGCTTCTCCAGGTGAGACTGGGTGGCCGCTCATGAAATCAACACGA 443
    |||||||
Db 144773 AGCCGACGAGAGCTTCTCCAGGTGAGACTGGGTGGCCGCTCATGAAATCAACACGA 144714

QY 444 GGCGGAGACCTTGAGACCTGTGTCCCGACGGGCTTCTACCTGGCCCTCCAGAGCTANGG 503
    |||||||
Db 144713 GGCGGAGACCTTGAGACCTGTGTCCCGACGGGCTTCTACCTGGCCCTCCAGAGCTANGG 144654

QY 504 CGGCTGACATGCTCCATGATGCGCTGTGCTTCTACCAAGTGGCCCCCGGATATCA 563
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Db 144653 CGGCTGACATGCTCCATGATGCGCTGTGCTTCTACCAAGTGGCCCCCGGATATCA 144594

QY 564 GAATGGCGCATCTTTCAGAGAAACCTGTGCGGGGGGTGAGACACATGCTGCTGCTGC 623
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Db 144593 GAATGGCGCATCTTTCAGAGAAACCTGTGCGGGGGGTGAGACACATGCTGCTGCTGC 144534

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QY 624 CCGGGGACGCTGATCCCAATGCGGAAGAGTGATGATCCATCAAGCTTACTGTAA 683
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QY 684 CCGGGGACGCGAGTGGCTGGTGGCCATCGGGCGCTGATGCAAGCAGCTTCAGGC 743
    |||||||
Db 144473 CCGGGGACGCGAGTGGCTGGTGGCCATCGGGCGCTGATGCAAGCAGCTTCAGGC 144414

QY 744 CGTTGAGATGCGACCGCTGCGGAGGT 771
    |||||||
Db 144413 CGTTGAGATGCGACCGCTGCGGAGGT 144386

RESULT 13
AL157403/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

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AL157403 111026 bp DNA HTG 23-JAN-2001
Homo sapiens chromosome 1 clone RP5-1158110 map p22.3-31.2, ***
SEQUENCING IN PROGRESS ***, 13 unordered pieces.
AL157403
AL157403.3 GI:9796550
HTG; HTGS_PHASE1; HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 111026)
Paylt,R.
Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9212375.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: d1158110
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ABI; 0% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Consensus quality: 105665 bases at least Q40
Consensus quality: 107614 bases at least Q30
Insert size: 109826; sum-of-contrigs
Quality coverage: 3.50x in Q20 bases; sum-of-contrigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 7499: contig of 7499 bp in length
* 7500 7599: gap of 100 bp
* 7600 10440: contig of 2841 bp in length
* 10441 10540: gap of 100 bp
* 10541 17763: contig of 7223 bp in length
* 17764 17863: gap of 100 bp
* 17864 33875: contig of 16012 bp in length
* 33876 33975: gap of 100 bp
* 33976 43661: contig of 9686 bp in length
* 43662 43761: gap of 100 bp
* 43762 52351: contig of 8590 bp in length
* 52352 52451: gap of 100 bp
* 52452 57434: contig of 4983 bp in length
* 57435 57534: gap of 100 bp

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* 57535 64699: contig of 7165 bp in length
* 64700 64799: gap of 100 bp
* 66400 67779: contig of 2380 bp in length
* 67780 67879: gap of 100 bp
* 67880 75753: contig of 7874 bp in length
* 75754 75853: gap of 100 bp
* 75854 84744: contig of 8888 bp in length
* 84744 84841: gap of 100 bp
* 84842 101025: contig of 16184 bp in length
* 101026 101125: gap of 100 bp
* 101126 111026: contig of 9901 bp in length.
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## FEATURES

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vector_side:left"
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fragment_chain:2"
33976. .43661
/note="assembly_fragment:01078
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43762. .52351
/note="assembly_fragment:00050"
52452. .57434
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57535. .64699
/note="assembly_fragment:00599"
64800. .67779
/note="assembly_fragment:01030"
67880. .75753
/note="assembly_fragment:00690
fragment_chain:3"
75854. .84741
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fragment_chain:3"
84842. .101025
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101126. .111026
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vector_side:right"
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Matches 251;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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DB	84408	CAGGGAGAGTTGGCAGGCTCAGTGGCCACTGAACTGGCAGGACAGAGACATCT	84344
QY	1898	TTGTGGCCATCAGACGCTCAAGTGGGGCTACACGGAGAACGAGCGGGACCTTCTTA	1957
DB	84348	TTGTGGCCATCAGACGCTCAAGTGGGGCTACACGGAGAACGAGCGGGACCTTCTTA	84285

Qy	1958	GCGAAGCCTCCATCATATGAGGCGAGTTGCAGCAATCCCAAGCTATCCAGCTGGAGGGGTGCG	2017
Db	84288	GGGAAGCCTCCATCATATGAGGCGAGTTGCAGCAATCCCAAGCTATCCAGCTGGAGGGGTGCG	84229
Qy	2018	TGACCAAGAGCACACCTGTGATGATCATCACCGAGTTCATGGAGAGTGGCTCCCTGGA	2077
Db	84228	TGACCAAGAGCACACCTGTGATGATCATCACCGAGTTCATGGAGAGTGGCTCCCTGGA	84169
Qy	2078	CCTTTCTCCGG	2088
Db	84168	CCTTTCTCCGG	84158

## RESULT 14

LOCUS	113956 bp	DNA	27-SEP-2000
DEFINITION	Human DNA sequence from clone RP1-74M1 on chromosome 1p34.3-36.13. Contains the EPHB2 gene for a protein tyrosine kinase. Contains ESTs, GSSs, STS and a CpG island, complete sequence.		
ACCESSION	AL035704	9	GI:6165330
VERSION	AL035704.1		
KEYWORDS	HTK; CpG island; EPHB2; tyrosine kinase.		
SOURCE	human.		
ORGANISM	Homo sapiens		

## ORGANISM

REFERENCE  
1 (bases 1 to 113956)  
Eukaryota; Eukarya; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS	Baguley, C.
TITLE	Direct Submission
JOURNAL	Submitted (27-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, UK

## JOURNAL

COMMENT  
On Oct 31, 1999 this sequence version replaced g1.605897.  
Data published here is generated from Superlattice clones  
requests: clonerequests@anger.ac.uk  
CB10 ISA, UK. E-mail enquiries: numquetyes@anger.ac.uk  
Clone

**COMMENT**

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unseq' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone compigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

RP1-74M1 is from the library RPci-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://dacpac.med.buffalo.edu/VECTOR:pcrpac2>

This sequence is the entire insert of clone RP1-74M1.

## FEATURES

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527. .624
  /note="MIR repeat: matches 47. .151 of consensus"
804. .861
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/ote="LIMBS repeat: matches 6129. .6172 of consensus"
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Em:IA3621 Em:IA1939 Em:Z19110 Em:L25890 Em:X76011
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Em:AA52367 Em:AI08197 Em:W64737 Em:W6506 Em:AI809403
Em:AA837292 Em:AA505599 Em:AA573757 Em:AI216739
Em:AI739658 Em:W73189 Em:AI445236 Em:AA622626 Em:AI268257
Em:AW162602 Em:AA505740 Em:AA552072 Em:W27292 Em:AA570007
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30269. .30462,32331. .32486,33349. .33451,33545)
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Em:AF216799 Em:AF237766
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Em:W76439 Em:AI702993 Em:AI476586 Em:AM365103 Em:AA570007
Em:AM168439 Em:AI344182 Em:AI911816 Em:AI345870
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gene

CDS

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30269. .30462,32331. .32486,33349. .33451,33545)
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/ote="continues in dJ61A9 (AL035703), gene dJ61A9.1
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Sw:P29344 Tr:043569 Sw:P09759 Sw:P54762 Tr:007494
Tr:0291736 Tr:007498 Sw:P54754 Tr:091735 Sw:P54753
Sw:P207497 Tr:095143 Sw:P08060 Sw:P29317 Tr:09V4E5
Sw:P21709 Tr:09XZL6 Sw:P54761 Tr:09V4E5 Tr:09Y1Y3
Tr:09Y1J0 Sw:005688 Tr:091845 Tr:09V4E5 Sw:002466
Tr:09U8V3 Sw:P25911 Tr:091845 Tr:073876 Tr:091694
Tr:0291776 Sw:003145 Tr:008644 Sw:P07948 Tr:P88459
Sw:P10936 Sw:P29319 Sw:015197 Tr:P79726 Tr:013332
Tr:063130 Tr:073875 Tr:09VUC8 Tr:063132 Tr:060705
Sw:P08922 Tr:093596 Sw:060750 Tr:09V4V5 Sw:P42689
Sw:P42687 Tr:093596 Tr:093597 Sw:P42685 Sw:007496
Tr:093457 Tr:09V5E2 Tr:09V5E2 Tr:091433 Sw:062413
Tr:026299 Tr:099082 Sw:P00526 Sw:P08125 Tr:042362
Tr:007912 Tr:01850 Sw:007407 Sw:P0736 Sw:P00527
Sw:P29318 Tr:0905Y2 Sw:P07949 Tr:09XEL3 Tr:09U7P9
Tr:013064 Sw:002080 Tr:013147 Tr:09VD94 Sw:003137
Tr:09PVV0 Sw:P09324 Tr:09PVV1 Tr:09PVV2 Tr:081485
Tr:090478 Tr:026639 Sw:P32577 Sw:P14616 Tr:09SWF1
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CDS

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DB 26714 GCGAAGCTCCATCATGAGGCGCAGTTCGACCATCCCAAGCTCATCCAGCTGAGGGGTGCG 26773  
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QY 2078 CCTTCTCCGG 2088  
DB 26834 CCTTCTCCGG 26844

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DEFINITION 22 unordered pieces.  
AC067727  
VERSION AC067727.5 GI:9438548  
KEYWORDS HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
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Muzny, D.M., Adams, C., Bailey, M., Barbara, J., Blankenburg, K.,  
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Taber, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M.,  
Washington, S., Weinstein, G., Weinstein, I.R., Williamson, A.,  
Worley, K., Wren, J., Wrenford, G., Yu, W., Zhou, X., Nelson, D. and  
Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 149709)

Submitted (27-APR-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Jul 25, 2000 this sequence version replaced gl:8699853.  
COMMENT

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center project name: HAXB  
Center clone name: RP11-6916  
Sequencing vector: M13; L08821

Chemistry: Dye-terminator Big Dye: 53% of reads  
Assembly: Phrap; version 0.990329  
Consensus quality: 144887 bases at least Q40  
Consensus quality: 144887 bases at least Q30  
Estimated insert size: 142903; sum-of-coverage estimation  
Quality coverage: 3.4x in Q20 bases; agarose-gel estimation  
Quality coverage: 3.4x in Q20 bases; sum-of-coverage estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 22 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 32213: gap of unknown length  
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\* 51392: gap of unknown length  
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\* 101019: contig of 6359 bp in length  
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\* 117531: contig of 3833 bp in length  
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\* 141057: gap of unknown length  
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\* 142974: gap of unknown length  
\* 144613: contig of 1540 bp in length  
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\* 146827: contig of 2113 bp in length  
\* 146926: gap of unknown length  
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\* 148595: gap of unknown length  
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Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 47714 CAGGGAGTTTGGCGAGTCTGCGACCTGGAAGCTGCCAGGCAAGAGAGATCT 47655  
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QY 1898 TTGTGGCCATCAAGACGCTCAAGTGGGCTACACGGAGAAAGCGCCGGACTTCTGA 1957  
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Db 47534 TGACCAAGACACACCTGTGATGATCATCACCGAGTTTCATGAGAAATGGCTCCCTGGACT 47475  
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QY 2078 CCTTTCTCCGG 2088  
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Db 47474 CCTTTCTCCGG 47464  
|||||

Search completed: July 10, 2001, 21:29:08  
Job time: 10270 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 18:41:48 ; Search time 195.34 Seconds  
(without alignments)  
9521.064 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CCGCTCGCGCGCGCTGAGAGA.....CCAAAGCCCGCCCTCTCTGCG 2962

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 730101 seqs, 313950809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N.Geneseq\_0601.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2962	100.0	2962	16	AA02946
2	2233	75.4	3949	21	AAA88549
3	1996	67.4	3768	21	AAA88548
4	1673	56.5	3151	21	AAA09322
5	120	4.1	171	16	AA096250
6	85	2.9	381	14	AA060025
7	48	1.6	3105	16	AA07308
8	48	1.6	3105	16	AA084528
9	32	1.1	3776	16	AA090655
10	30	1.0	3751	16	AA063461
11	29	1.0	3133	15	AA090652

12	29	1.0	3592	20	AAV70208	Rat receptor tyros
13	29	1.0	4049	16	AA090660	Eph-related PTK Ce
14	29	1.0	4097	16	AA090657	Eph-related PTK Ce
15	26	0.9	1509	14	AA053470	PTK gene Bl. Ratt
16	26	0.9	4281	14	AA053471	elk CDNA. Rattus
17	25	0.8	39	16	AA02951	HEK5 extracellular
18	25	0.8	81	13	AA030727	Potential tyrosin
19	25	0.8	81	20	AAV70222	Rat orphan tyrosin
20	25	0.8	3546	16	AA090656	Eph-related PTK Ce
21	25	0.8	3591	16	AA090658	Eph-related PTK Ce
22	25	0.8	3591	16	AA090658	HEK5 extracellular
23	24	0.8	54	16	AA02950	Elk receptor signa
24	24	0.8	3669	14	AA049757	PTK gene HprtK5. H
25	24	0.8	3969	16	AA03099	Protein tyrosine-k
26	24	0.8	4290	16	AA092641	Human non-differen
27	24	0.8	4290	17	AA042593	Coding sequence fo
28	24	0.8	4290	17	AA042593	Receptor type tyro
29	24	0.8	4290	17	AA042593	Receptor type tyro
30	23	0.8	171	19	AAV55890	Receptor protein t
31	23	0.8	171	20	AAV55890	Receptor protein t
32	23	0.8	2170	20	AAZ41307	Human normal ovar
33	23	0.8	2982	16	AA090971	Protein p140 CDNA
34	23	0.8	3056	16	AA090662	Eph-related PTK Ce
35	23	0.8	3059	16	AA090653	Eph-related PTK Ce
36	23	0.8	3125	16	AA090661	Eph-related PTK Ce
37	23	0.8	4027	16	AA090972	Protein p140 CDNA
38	23	0.8	4027	16	AA090982	Protein p140 CDNA
39	22	0.7	171	19	AAV55891	Receptor protein t
40	22	0.7	171	20	AAV55891	Receptor protein t
41	21	0.7	21	22	AAV55891	Human gene single
42	21	0.7	21	22	AAV55891	Human gene single
43	21	0.7	3162	16	AA02947	Eph-like receptor
44	20	0.7	171	19	AAV55896	Receptor protein t
45	20	0.7	171	20	AAV55896	Receptor protein t

#### ALIGNMENTS

RESULT 1	
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ID	AA02946 standard; cDNA; 2962 BP.
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AC	AA02946;
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DT	16-APR-1996 (first entry)
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DE	Eph-like receptor protein tyrosine kinase HEK5 CDNA.
XX	
KW	Eph-like receptor protein tyrosine kinase; PTK; HEK5;
KW	human eph-like kinase; therapy; diagnosis; antibody; vector; ss
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
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PN	W09528484-A1.
XX	
PD	26-OCT-1995.
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PF	14-APR-1995; 95WO-US04681.
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PR	15-APR-1994; 94US-0229509.
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PA	(AMGE-) AMGEN INC.
XX	
PI	Fox GM, Jing S, Welcher AA;
XX	
DR	WPI: 1995-373799/48.
DR	P-PSDB; AAR85089.
XX	

PT New nucleic acid encoding Eph-like receptor tyrosine kinase(s)  
PT and related vectors, host cells, proteins, antibodies etc., used  
PT diagnostically and therapeutically to modulate receptor activation  
or prodn.

PS Claim 1; Page 41-45; 133pp; English.

XX cDNAs (AA02946-49) coding for 4 novel human Eph-like receptor protein  
CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (AAR5089-92),  
CC respectively, were isolated from a human foetal brain cDNA library using  
CC a directed PCR approach with primers (see AA02960-61) based on conserved  
CC regions of receptor PKTs and Eph-like receptor PKTs. HEK5, HEK7 and HEK8  
CC show extensive homology to the catalytic domain of chicken Eph-like  
CC receptors Cex5, Cex7 and Cex8. HEK11 shows no homology to any known  
CC Eph-like receptor. The isolated cDNAs are used for prodn. of  
CC recombinant HEKs and chimeric receptors, in hybridisation assays, and  
CC to detect abnormalities in HEK receptor genes.

SQ Sequence 2962 BP; 654 A; 914 C; 827 G; 567 T; 0 other;

Query Match 100.0%; Score 2962; DB 16; Length 2962;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 tggatgagtgatcctcatcatgaggtggagaagtgagtgagctcagatgagaataaac 120
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DB 301 tactatagagctgactttgactggccaccagacttcccaactggatgagatca 360
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DB 481 tactgagcttctcagagcatttgcgcggtgatgctcctcatccgcggtgcttcttac 540
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DB 721 atgtcaagacgagcgcttgagagcggcttgagaaatggacaccgctctccgagtggtgcatt 780
QY 781 GGGACTTTCAAGGCGCAACCAAGGGGATGAGCGCTGTACCCACTGTGCCATCAACAGCCGG 840
DB 781 gggactttcaaggcgcaaccaagggatgagcgctgtacccactgtgccatcaacagccgg 840
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DB 841 accacttctgagagcgccaccactgtgtgtcggcgcaatggctctacagacgagactg 900
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DB 901 gacccctgacatacctctgatgctggagtggacccctcccggaactccgaggccgagag 1020
QY 961 GTCAATGAGACTCTCTCATGCTGTGGAGTGGACCCCTCCCGGCACTCCGAGGCCGAGAG 1080
DB 961 gtcaatgagactctctcatgctgtggagtggacccctcccggaactccgaggccgagag 1080
QY 1021 GACCTGCTACACATCATCTGCAAGAGCTGTGGCTGGGGCGGGGTGCTGCACCCGC 1080
DB 1021 gacctgctacacatcatctgcaagagctgtggctggggcggggtgctgcacccgc 1080
QY 1081 TCGCGGAGCAATGTACAGTACGACACACGACGCTAGGCGCTGACCGACGACCATTTAC 1140
DB 1081 tcgcggagcaatgtacagtacgacacacgacgctaggcgctgacccgacacatttac 1140
QY 1141 ATCAGTACGCTGCTGCGCCACACCCATACACCTTCAGAGATCCAGAGTGGAGCGGCTT 1200
DB 1141 atcagtacgctgctgcgccacacccatacaccttcagagatccagagtggaagcgctt 1200
QY 1201 ACTGACACGAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 actgacacgagcccttctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1260
QY 1261 GCTTCATCGGACGATGTGCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 gcttcacggacgatgtgctcatgatgatgatgatgatgatgatgatgatgatgatgatgat 1320
QY 1321 TCGGTGCTCCAGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1380
DB 1321 tcggtgctccagcggacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 1380
QY 1381 GAGAGAGGCTCAGTGAATCAACGCGCACAGCCATAAAGGCCCAACCAACAGGCTACG 1440
DB 1381 gagagaggctcagtgaatcaacgcgcacagccataaaggcccaacccaacagctacg 1440
QY 1441 GGCCTCAAGCGCGGCGCATCTATGCTTCCAGTGGGGGACGACGCTGGAGGCTTAC 1500
DB 1441 ggcctcaagcgcgcgcatctatgcttccagtgggggacgacgctggaggcttac 1500
QY 1501 GGGCGCTACAGCGGCAAGATGATCTTCAGACCATGACAGACGACGATACCGAGAACG 1560
DB 1501 gggcgctacagcgcgcaagatgatcttcagaccatgacagacgacgataccgagaaacg 1560
QY 1561 ATCCAGGAGAGTTGGCAGTCATCATCGGCTCTCGGCGCTGCTGGCTTCTCTCATTT 1620
DB 1561 atccaggagagttggcagtcattcatcggtctcggcgctgctggcttctctcattt 1620
QY 1621 GCTGTGTTGTATGTCGATCGTGTGTAACAGAGGAGGTTTGAAGTGTGCTGCTGAGAG 1680
DB 1621 gctgtgttgtatgtcgtgtgtgtaacagaggggttgaagtgtgctgagag 1680
QY 1681 TACAGGACAGCTGCAACACTACACCAAGTGGCGACATAACCCAGAGCATGAAGATCTAC 1740
DB 1681 tacaggacagctgcaaacactacaccaagtggcgacataaacccagagcatgaagatctac 1740
QY 1741 ATGATCTCTTTCACCTACAGAGACGACGACGACGACGACGACGACGACGACGACGACG 1800
DB 1741 atgatctctttcacctacagagacgacgacgacgacgacgacgacgacgacgacgacgac 1800
QY 1801 GACATCTCTGTGTCAAAATTGAGAGGTGATCGAGCAGGAGGAGTGTGGAGGCTGCTGC 1860
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Db 1861 agtggccaccggaagcctgcgcagagcaagaagagatcttctgtggccatcaaaagcgtcaag 1920
Oy 1921 TCGGGCTACACGAGAAACAGCGCGCGGAGCTTCTGAGCAAGCCTCCATCATGGGCCAG 1980
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Db 2101 cagttcacagatcatccacgtctgtgggcaatgtctcggggcattcgacgtgcatagag 2160
Oy 2161 CTGGCAGACATGAACTATGTTACCGGTGACCTGGCTGCCCGCACATCTCTGTCAACAGC 2220
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Oy 2221 AACCTGCTCCTCAAGGTTGCTGGAGCTTTGGGCTCTCAGCCTTTCTAGAGAGAGATACCTCA 2280
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Db 2221 aaactggtctcgaaggtgtcggactctgtgactctcagctctctctcgaagagatgccca 2280
Oy 2281 GACCCACACTACACCAAGTGCCTGGCGGAAAGTCCCATCCGCTGCAACAGCCCCGAA 2340
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Db 2281 gaccacacctcaacacagctgacctggcgaaagtctcccatcgcgttggaacgccccgaa 2340
Oy 2341 GCCATCCAGTACCGGAATTTACCTCGGCAATGATGTTGAGAGTACGGCATTTCTCATG 2400
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Db 2341 gccatccagctccggaagltcaacctgcgacagtgatgtgtgagagctacggcatgtctac 2400
Oy 2401 TGGGAGTGTATGTCCTATGGGGAGCGGCCCTACTGGAGATACCAACAGAGATTAATC 2460
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Oy 2461 AATGCCATTGAGCAGAGATATCGGCTGCCACCGCCATGAGACTGCCGACGCCCTGCAC 2520
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Db 2461 aatgcattgtgcagagactatcgtgcacacgcccactgtgacctgcgagcgccctgcac 2520
Oy 2521 CAATCATGCTGAGACTGTTGGCAGAAAGACCGCAACACCGGCCCAAGTTGGGCCAATT 2580
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Db 2521 caactcatgtgtgactgtgtggagaagacgcgaacacacgcgcccgaaglttcgccaat 2580
Oy 2581 GTTCAACAGCTGAGCAAGATGATCGGCAATCCCAACAGAGCTCAAAAGCCATGGCCCTC 2640
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Db 2581 gtcaacacgctgagacaagatgtatccgcaatccccaaagcctcaaaagcctgtgcctc 2640
Oy 2641 TCCTCTGGCATCAACCTGCTGCTGTGACGCGACAGATCCCGACTACACAGCTTTTAAC 2700
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Db 2641 tccctctgcatcaaacctgcgtgtgtgacgcgcacgattccccgactcaacacagctttaa 2700
Oy 2701 ACGGTGACAGATGCTGTGAGGCGCATCAAGATGGGCACTACAAAGAGAGCTTCCCAAT 2760
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Db 2701 acggtgagcaggtgtgtgtgagggcctcaagatggtgtgagagaggtctgcctcaat 2760
Oy 2761 GCGGCTTACACTCTCTTGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 2820
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Db 2761 gccggcttcaacctctctgagcgtgtgtctcagatgataagagacatctccgggtt 2820
Oy 2821 GGGGTCACTTTGGCTGGCCACGAGAAAATCTGAACAGTATCCAGGTGATGGCGGC 2880
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Db 2821 ggggtcaacttgcgtgcgcacagaaaaatctctgaacagatcatcaggtgtgtgcgg 2880
Oy 2881 CAGATGAACCAATTCAGTCTGTGAGGTGTTACATTCACCTGCTCGGCTACCTCTTC 2940
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Db 2881 cagatgaaccagatcatcgtctgtgaggtttgacatcacctgtcgtcctacattctc 2940
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Db 2941 ctccaagccccgccctctgc 2962

RESULT 2
AAA88549
ID AAA88549 standard; cDNA: 3949 BP.
XX
AC AAA88549:
XX
DT 22-JAN-2001 (first entry)
XX
DE Human CASB616 cDNA.
XX
KW CASB616; EPHB2; ERK; EPH3; EPH3.3; DRT; HEK5; EPHB2V;
KW receptor protein tyrosine kinase; human; antigen; colon cancer;
KW ovary cancer; tumour; autoimmune disease; vaccine; gene therapy;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 26..3193
FT FT /*tag= a
XX
XX WO200053216-A2.
XX
XX 14-SEP-2000.
XX
XX 28-FEB-2000; 2000WO-EP01587.
XX
XX 05-MAR-1999; 99GB-0005124.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Vinals De Bassols VC;
XX
XX WPI: 2000-587384/55.
XX
XX P-PSDB: AAB19591.
XX
XX Vaccine composition for treating ovarian and colon cancer, comprises
XX CASB616 polypeptides, polynucleotides or antigen presenting cells
XX expressing the polypeptides
XX
XX Claim 3; Page 41-42; 57pp; English.
XX
XX The present sequence is that of cDNA coding for human CASB616 (see
XX AAB19591), a member of the EPH and EPH-related family of receptor
XX protein tyrosine kinases. CASB616 is also known as EPHB2, ERK,
XX EPH3, EPH3.3, DRT, HEK5 and EPHB2V. CASB616 polypeptides and
XX polynucleotides are important immunogens for specific prophylactic
XX or therapeutic immunization against tumours, especially colon
XX cancer (claimed) and ovarian cancer. They are specifically
XX expressed or highly over-expressed in tumours compared to normal
XX cells and can thus be targeted by antigen-specific immune
XX mechanisms leading to destruction of the tumour cells. They can
XX also be used to diagnose the occurrence of tumour cells. Their
XX inappropriate expression can also cause an induction of autoimmune
XX responses, which can be corrected through vaccination using the
XX CASB616 polypeptides or polynucleotides.
XX
XX Sequence 3949 BP; 934 A; 1142 C; 1105 G; 768 T; 0 other;

Query Match 75.4%; Score 2233; DB 21; Length 3949;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Oy 1 CTGTCGCGCGCGGTGAGAAACGCTAATGAGCTCACTACAGCGAGCTGAGTGGGC 60
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Oy 2215 AACAGCACTGCTGTGCAAGGTGTGCGACTTTGGGCTCTACGCTTTTCTAGAGGACGAT 2274
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Db 2288 aacagcaactgctgtcgaagtgctcgacttgggtctcaacgcttctcagaagagacat 2347
Oy 2275 ACCTGACACCCCACTACACAGTGGCCCTGGGGAAGTTCCCATCCCTGGACAGGC 2334
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Db 2348 accctaaccccccctacacacagtcggtcggaagaatcccaaccgctcgagcgc 2407
Oy 2335 CCGGACGACCTACGATACCGGAAGTTACCTCGGCGAGTATGTGTAGACTACGCGATT 2394
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Db 2408 ccggaagccatcccgatcccggaagttcaactcgcgcagtgatgtgtgagctaaagcatt 2467
Oy 2395 GTCATGTGGAGGTGATGTCTATGGGAGCGGCCCTACTGGGACATACCAACAGCAT 2454
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Db 2468 gctatgtggaggtgtatgtctcctatgggagcggtccctactggtgacatgacaaacagat 2527
Oy 2455 GTATCAATGCCATTGACGAGCATATCGGCTGGCCAGGCCCATGAGACTGGCCGAGCGC 2514
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Oy 2515 CTGCAACCACTATGCTGAGACTTTGGCAGAGAGCAGCAACACCGGCCCAAGTTGCGC 2574
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Db 2588 ctgcacacactcatgtcgtgactgtgttcgagaagaagccgcaaccccgcccaagttcgcg 2647
Oy 2575 CAAATTGTCAACAGCTAGAGACAGATGATCCGCAATCCCAACAGCTCAAAAGCATGGCG 2634
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Db 2648 caaatgtcaaacacgctagacaagatgattccgcaatcccaacagctcaaaagcattgagcg 2707
Oy 2635 CCCCTCTCTTGGCATACACCTGCTGTGTGACCCGACGATCCCGACTACACAGC 2694
    |||||||
Db 2708 cccctctctctgtgcatcaacacctgcgtctgacgcgacagatcccgactacaacagc 2767
Oy 2695 TTTAAACAGGTGGAGAGTGGCTGGAGCCATCAAGATGGGCGGACTACAAAGAGAGCTTC 2734
    |||||||
Db 2768 tttaacacggtgagcaggtgtgtgagagccatcaagatgggagcgtataaagagaagcttc 2827
Oy 2755 GCCAATGCGGCTTACCTCTTGTGACGTCGTGTCTCAGATGATGATGAGGACATTTC 2814
    |||||||
Db 2828 gcaaatgacggtctcaactcctcttgagctgtctcagatgatatgagagacattctc 2887
Oy 2815 CGGGTGGGGTCACTTTGGCTGGCCACCAAGAAAAATCTGAAAGATTCAGGTGAGTG 2874
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Db 2888 cgggctgggtgactcttggtcgtgacccagaaaataatccctgaacagatcccaagtgatg 2947
Oy 2875 CGGGCGAGATGAACCAAGATTCACTGTGTGGAG 2908
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Db 2948 cgggcgcagatgaacacagatcagctgtgtgagag 2981

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Pd 14-SEP-2000.
Xx
Xx 28-FEB-2000; 2000WO-EP01587.
Xx
Xx 05-MAR-1999; 99GB-0005124.
Xx
Xx (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
Xx
Xx Vlnals De Bassols YC;
Xx
Xx WPI; 2000-587384/55.
Xx
Xx P-PDB; AAB19590.
Xx
Xx Claim 3; Page 40-41; 57pp; English.
Xx
Xx The present sequence is that of cDNA coding for human CASB616 (see
Xx AAB19590), a member of the EPH and EPH-related family of receptor
Xx protein tyrosine kinases. CASB616 is also known as EPHB2, ERK,
Xx EPH3, EPHB3, DRT, HEK5 and EPHB2V. CASB616 polypeptides and
Xx polynucleotides are important immunogens for specific prophylactic
Xx or therapeutic immunization against tumours, especially colon
Xx cancer (claimed) and ovarian cancer. They are specifically
Xx expressed or highly over-expressed in tumours compared to normal
Xx CC cells and can thus be targeted by antigen-specific immune
Xx CC mechanisms leading to destruction of the tumour cells. They can
Xx CC also be used to diagnose the occurrence of tumour cells. Their
Xx CC inappropriate expression can also cause an induction of autoimmune
Xx CC responses, which can be corrected through vaccination using the
Xx CC CASB616 polypeptides or polynucleotides.
Xx
Xx Sequence 3768 BP; 872 A; 1129 C; 1058 G; 709 T; 0 other;
Xx
Xx Query Match 67.48; Score 1996; DB 21; Length 3768;
Xx Best Local Similarity 99.58; Pred. No. 0;
Xx Matches 2956; Conservative 0; Mismatches 6; Indels 9; Gaps 2;
Xx
Xx 1 CTGCTGGCGCGCGTGGGAAGAACCTAATGAGTACCTACAGCGAGCTGTGAGCTGGC 60
Xx 147 ctgctgcgcgcgcgtgggaagaacctaatgagctaccctacagagactgtcgtgagctggc 206
Xx 61 TGGATGTGATCTCTCCATCAGGTGGAGAGGTGATGCTACGATGAGACATGAAAC 120
Xx 207 tggatgtgactctctccatcaggttgggaagaggtgagtgagctacgtatgagaacatgaac 266
Xx 121 ACGATCCGACAGTACAGAGTGTGCAAGCTGTTTGTAGTCAACCGAACAATGGCTACGG 180
Xx 267 acgatccgacagtgaccaggtgtgcaagctgtttagtcaaacccgaacaaactggtcagg 326
Xx 181 ACCAAGTTATCCGCGCGGTGGGCGCCACCGACGATCCACGTGAGATGAAGTATTTGGGTG 240
Xx 327 accaagttatccgcgcggtgggcccacccgacatccacgctgagatgaagtttcggtg 386
Xx 241 CGTGAATGACAGCATCCACAGCGTGTGCTGTCTGCAAGAGAGACTTAACTCTAT 300
Xx 387 cgtgaatgacagcatccacagcgtgtgtcctctgcaagagaaaccttaaacctctat 446
Xx 301 TACTATGAGCGTGATTTGATCGGCGACCAAGACCTTCCCACTGATGATGAGATCA 360
Xx 447 tactatgagcgtgacttggactcggccacaaagactctcccaacttgaatggaatcca 506
Xx 361 TGGGTGAAGGTGATATCACTGACGCGACGAGAGACTTCTCCAGTGGAGACTGGGTGGC 420
Xx 507 tgggtgaaggtgatattcactgacgctgacgagcgttctcccaagtgagacttgggtggc 566
Xx 421 CGCGTCAAGAAATCAACACGAGGTGGCGAGCTTGGAGACTGTGTCCCGACGCGGCTTC 480
Xx 567 cgcgtaagaaatcaacacaggttggagagcttcgagacttgggtggcgtggcgttc 626

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RESULT 3
AAA88548
ID AAA88548 standard; cDNA; 3768 BP.
XX
XX AAA88548;
XX
XX 22-JAN-2001 (first entry)
XX
XX Human CASB616 cDNA.
XX
XX CASB616; EPHB2; ERK; EPHB3; EPHB3; DRT; HEK5; EPHB2V;
XX receptor protein tyrosine kinase; human; antigen; colon cancer;
XX ovarian cancer; tumour; autoimmune disease; vaccine; gene therapy;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 105..3068
XX FT /*tag= a
XX FT /transl_except= (pos:2973..2975,aa:Leu)
XX
XX W0200053216-A2.

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QY 541 CGCAAGTGGCCCCGATCATCATCAAAATGGCGCATTTTCCAGAAACCTGTGCGGGCT 600  
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Db 687 cgaagtgccccgcgcatatccaaatgagcgcatcttccegaanaaccctgtcggggct 746  
QY 601 GAGAGCATATGCTGTGGTGGTGGCGGCGAGTGCATGCGCAATGGGAAAGAGTGGAT 660  
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Db 747 gaggagcaatcgctggtgctgcgccggggcagctgcgcatcgcaatgcggaagagtgat 806  
QY 661 GTACCCATCAAGCTCTACTGTATACGGGGACGGCGAGTGGCTGTGTCATCGGCGCTGC 720  
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Db 807 gtaccatcaagctactactgtaacgaggacgagcgatgctgtggtccatcgcgctgc 866  
QY 721 ATGTCAAAGAGGCTTCGAGGGCGGTGAGAAATGGCACCGCTGCGCAGGTGTGCTCT 780  
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Db 867 atgtgcaaaagcaagcttcgagggccgttgagaatgagcagctgtcgaggtgttcacatc 926  
QY 781 GGGACTTTCAAGGGCCAAACAAAGGGATGAGGGCTGTACCCACTGTCCATCAACAGCCG 840  
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Db 927 gggagcttcaagggcaaccaaaggagatgagcgctgtaccatcgctccacaagaagccgg 986  
QY 841 ACCACTTCTAAGGGGCGCCACCAACTGTGTCTCGCGAATGGCTACTACAGAGCAGCTG 900  
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Db 1707 acaagctccagagagaagtggtccatcatatcgctcccgccgctggtccgtcttc 1766  
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Db 1767 ctcatgtctgtgtgtgtcatcgccatcggtgtgttaacagaagagcggtgtgtgagcgctgc 1826  
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QY 1792 AAGGAATTACATCTCTCTGTCAAAATTTAGCAGAGTGTATCGAGCAGGAGGATTTGGC 1851  
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Db 1947 aaggaaatltgacatctccctgtgtcaaaatltgacagatgatacgagcagggaggttggc 2006  
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Db 2067 acgctcaagtcgggtgtacacggaggaagcagcgccgagcttccctgagcgagcctcatc 2126  
QY 1972 ATGGGCGAGTGCACCATCCCAACGCTATCCACTGAGAGGAGTGTGCTGACCAAGACACA 2031  
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Db 2127 atgggcagctgcacatcccaagctacacacatgagaggtgtgtgtgacaaagacaca 2186  
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Db 2187 cctgtatgatacatcacagagatgacagatgagatgagctccctgtgaccccttcgggcaa 2246  
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Db 2367 gtcaacgaacactgtgtcgaagatgtgcagcttgggtcttcagcttcttaagaagac 2426  
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QY 2392 ATTGTATGTGGGAGTGTGCTATGAGGAGCGGCTTATGGGAGATGAGCAACAGC 2451  
|||||  
Db 2547 atgtgcatgtggaggtgagtgctccatggtggcggtccctactgtggaatgacaaag 2606  
QY 2452 GATGTAAATCAATGCAATTGAGCAGAGCTATCGGCTGCCACCGCCATGAGTGCAGCAG 2511  
|||||  
Db 2607 gatgtaatcaatgcatltgagcagatcatgctgcgccaacgcccatagtgctccgggc 2666  
QY 2512 GCCCTGCACCACTATGCTGTGACTGTGTGGCAGAAAGACCGCAACCCAGCCCAAGTTC 2571  
|||||  
Db 2667 gccctgcaccaactatgtctgagctgtgtgcagaaagacgcgaacacagcccaagctc 2726  
QY 2572 GGCCAAAATTGTCAACAGCTAGACAAGATGATCCGCAATCCCAACAGCTCAAAAGCCATG 2631  
|||||  
Db 2727 ggcgaatltgtcaacagctagacaaagatgatactgcgaatcccaagcctcaaaagctc 2786  
QY 2632 GCGCCCTCTCTCTGTGGATCAACCTGCCGCTGTGAGCCGACAGATCCCGCATACACC 2691  
|||||

Db	2718	gcgcacctctctccctcgtgacatcaaacctgcgcgcctcgtcgtgacgcagcaatccccgactaaccc	2846
Oy	2692	AGCTTTAACACGGTGGACAGTGGCTGGAGGCCATTCAGATGGGGCACTAGTACAAGACAGC	2751
Db	2847	agccttcaacacggtcggacagatcgtgcctggagagccatacaagatggggcagtaacaagagagac	2906
Oy	2752	TTCCGCATATCCGCGCTTCACCTCTTGGACGTCGTCATCATGATGATGAGAGACATT	2811
Db	2907	ctgcgcacaaigtgcgctctcaacctctcttgcgcgcgtcgcgtctccagatgatatgagagaaat	2966
Oy	2812	CTCCGGGTTGGGTCACATTGGCTGGCCACACAGAAAAAATCTTAACAGTATCCAGTG	2871
Db	2967	ctccgggtctgggctccactcttgcctctggccacacagaaataaaatcttcacagatcccaagt	3026
Oy	2872	ATGGGGGCGAGATGTAACACAGATTTCAGTGTGTGGAGGTTTGACATTCACCTGCGCGCT	2931
Db	3027	atgggggcgcagatgtaaaccaagatactgctgtggagaggttttgacatcaaacctgcgcctgcgt	3086
Oy	2932	CACCTCTTCTCTCCAGGCCCGCCCGCTCTGCG	2962
Db	3087	cacctctctctccaagcccgcccgccctctcgc	3117

RESULT 4  
 AAA09322  
 ID AAA09322 standard; DNA: 3151 BP.  
 AC  
 XX AAA09322;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Human cancer associated antigen precursor DNA, clone NY-REN-47.  
 XX  
 KW renal cancer; cancer associated antigen precursor; diagnosis;  
 KW cytosolic; ERK tyrosine kinase; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200020567-A2.  
 PN  
 PD 13-APR-2000.  
 XX  
 XX  
 PF 04-OCT-1999; 99WO-US22873.  
 XX  
 PR 05-OCT-1998; 98US-0166300.  
 PR 05-OCT-1998; 98US-0166350.  
 XX  
 PA (LUDWIG-) LUDWIG INST CANCER RES.  
 XX  
 PI Obata Y, Gout I, Tureci O, Sahin U, Pfeundschnub M, Scanlan MJ;  
 PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A;  
 XX  
 DR WPI: 2000-303774/26.  
 XX  
 PT Preventing, diagnosing and/or treating disorders associated with  
 PT abnormal expression of human cancer associated antigens  
 XX  
 XX Claim 57; Page 93-94; 121pp; English.  
 PS  
 XX  
 CC AAA09321-45 were isolated by SEREX screening from a renal cancer  
 CC cell line 1973/10.4. Homology searching revealed that these clones  
 CC correspond to known genes. The present sequence has identity with the  
 CC ERK tyrosine kinase gene. The genes encode cancer associated antigen  
 CC precursors. These gene products are useful in methods for preventing,  
 CC diagnosing and/or treating disorders, especially cancer, associated with  
 CC abnormal expression of human cancer associated antigens. The method  
 CC comprises contacting a sample from a subject with an agent that  
 CC specifically binds to the nucleic acid molecule or expression product  
 CC (or fragment) complexed with a human leukocyte antigen (HLA) molecule  
 CC and determining the interaction between the agent and the nucleic acid  
 CC molecule or the expression product as a determination of the disorder.  
 XX  
 SQ Sequence 3151 BP; 707 A; 974 C; 874 G; 596 T; 0 other;

Query Match	56.5%:	Score 1673:	DB 21:	Length 3151:
Best Local Similarity	99.3%:	Pred. No. 0:		
Matches 2933:	Conservative	0:	Mismatches 12:	Indels 9:
				Gaps 2:
QY	18	AGAAAGCGTAAATGAGACTCCATCCATACAGCGCACTGCTAGAGTGGGCTGGATGGTGCATCTCC	77	
Db	66	agaaacgctaatgagcttcacactacacagcgactctgagctcggtctgtagtgcatctccc	125	
QY	78	ATCAGGGTGGGAAGAGGTGATGCGCTTACGATATGAAACATGAACACGATCCGACGTACCA	137	
Db	126	atcaaggtcgtggaagaggtgtagtgcctacga tgaagaaca tgaacaacgattccgcagctacaa	185	
QY	138	GGTGTGCAACGGTGTGATGATCAAGCCAGAAACAATGGGCTAACGACCAAGTTTATCCGGCG	197	
Db	186	gtctgtcaacagtgtcttgtagtcaagccagaacaacactcgtctacgacaagaattcatccggcg	245	
QY	198	CCGTGGGGCCCAACCGCATCCACAGTGGAGATGAATTTTCGTGGTGGTGTACGACAGCAT	257	
Db	246	cgtgtgcgccccacgcgcatccacgctgagatgttctcgtgtcgtgtacgtcagcagcat	305	
QY	258	CCCCAGCGCTCCGGGCTCCTGCAAGAGACCTTCAACCTCTTTACTATAGAGGTACAT	317	
Db	306	ccccagcgtccctcgtctccctcgaagagaccttcaacccctatctactatgtaggcct	365	
QY	318	TGACTTCGGCCACAAGACACTTCCCAACTCGATGAGAAATTCATGCGGTGAAGGTGATAC	377	
Db	366	tgaactcgcgcacacaaagaccttcccacaactgga tgaagaa tcaatgggtgaaggtgaa taa	425	
QY	378	CATTCCAGCCGACGACGAGAGCTTCTCCAGGTGAGACCTGGGTGGCCCGCGCTATGAAATCA	437	
Db	426	catctcaacgcgcgcagagagctcttcccaag tgaacctggaacctggctgaac tgaataatcaa	485	
QY	438	CACCCAGGAGCGAGCTTCGAGACTGTGTGCCGACGCGCTTACTAGGCTTCCAGGA	497	
Db	486	caccgaagttcggaagctcttcgaacctgtgtcccgcaagcgactcttcaaccttcgaag	545	
QY	498	CTATGGCGGCTCATGTCCCTCATCGCCGTCGTGTCTTCTACCCGAGTGGCCCGCAT	557	
Db	546	ctatgtgcgctcga tgcctcatcgcg tgcgtgtctctcaacgaaatgc ccccgcat	605	
QY	558	CATCCAGATGGCGGCATCTTCCAGGAAACCTGTTCGGGGGCGTGAAGACATCGGTGG	617	
Db	606	catccagaat tgcgcacatcttccaaagaaacccgttcggggccgaagaa caacatcgctcgtc	665	
QY	618	GCGTCCCGCGGAGCTGCTGATCGCAATCCGGAAGAGTGGATGTACCATCAAGCTCTA	677	
Db	666	gctctgcgcgggcagctgcatacgcgaatgcggaaggtgtga tgcataccatcaagctcta	725	
QY	678	CTGTAAACGGGGACGGCGAATGGCTGGTGGCCATCGGGCGCTGCATGTGCAAGCAGGTT	737	
Db	726	cgttaacggggacggcgag tgcctgtgtgcacatcgggcgtgcga tgtgcaaaacaggtc	785	
QY	738	CGAGGCGGTGGAATGGACCGCTGCGGAGGTTTCCATCTGGGACTTCAAGGCCAA	797	
Db	786	cgaaagcgtctggaatgtagaacgctcgcgcgaaggttgttccaatcgtggaacttcaaggcaca	845	
QY	798	CCAAGGGATGAGGCGCTGTACCCACTGTCCATCAACAGCCGAGCACTTCTGAGGGCG	857	
Db	846	ccaagggatgtaggacctgtaccacaactgtcccatcaaacagccgaacacactcttbaagggc	905	
QY	858	CACCAACTGTGTCTGCGCGAATGGCTACTTACAGAGAGACACTGGACCCCTGGACATGGC	917	
Db	906	caccaactgtgtctgcgcgaatgtagctactacagaaagacac tggaccctctgaaabgc	965	
QY	918	CTGCAACAACATCCCTCCGCGGCCAGGCTGTGATTTCCAGTGTCAATGAGACTCCCT	977	
Db	966	ctgcacaacacatccctctcgcgcgcgaagcgtgtgattctcaagtgttcaatgtagacctccct	1025	
QY	978	CATGCTGAGTGGACCCCTTCCCGGACACTTCGGAAGCCGAGAGGACCTGCTCTAACAAAT	1037	
Db	1026	catgtctgaggtgtagacccctccgcgcgactctccgaaagccgaagaaagactcgtctcaacaat	1085	

QY 1038 CATCTGAAAGCTGTGGCTCGGGCCGGGGTGCCTGCACCCCGCTGCGGGACAAATGTACA 1097  
 |||||||  
 Db 1086 catctgaagagctgtgtctcgggccgggtgctgtcacccgcgtcggggaacaattgaca 1145  
 QY 1098 GTACGCAACCGCAGCTAGGCGCTGACCGACCAAGCAATTTACATCATGTAACCTGCTGGC 1157  
 |||||||  
 Db 1146 gtacgcacacagccagctagccctgacagcagcagcattacacgtgtacctgctgyc 1205  
 QY 1158 CCACACCACTAGCACTTTCAGATCCAGGCTGTGAAGCGGCTTACTGACGAGCCCTT 1217  
 |||||||  
 Db 1206 ccaacaccagtaaacctcttgagatccaggtgtgaaecggcttacctgacagagccctt 1265  
 QY 1218 CTGCGCTCACTTGCCTTGTGTGAACATCACACCAACAGGAGCTTCATCGGCAAGTTC 1277  
 |||||||  
 Db 1266 ctgcctcagctcgctctgtgaaacatcaccaacacagcagctccatccgcaagtgc 1325  
 QY 1278 CATCATGCAATCAGGTGAGCCGCGACCGTGGACAGCATTAACCTGTGCTGTCCAGCCGGA 1337  
 |||||||  
 Db 1326 catcatgcatcagtgtagccgacccgtgacagcattacccctgtgtgtccagccaga 1385  
 QY 1338 CCAGCCCAATGGCGTATCCTTGACTATGAGTGCAGTACTATGAGA--AGGAGCTCAG 1394  
 |||||||  
 Db 1386 ccagcccaatggtgtgtatctgtgacctatgagctgcaqlactatgagaagcagagctcag 1445  
 QY 1395 TGAATCAACGCGCACAGCCATAAAAAGCCCAACACAGGTGAC-----GGGCTCAA 1448  
 |||||||  
 Db 1446 tggatcaacgcacacagccataaaagcccaacaacgcgtgacaggtgagggctcaca 1505  
 QY 1449 AGCGGCGCATTTATGTCTTCCAGTGGCGGCGACGACATGTGGAGGCTACGGGGGCTA 1508  
 |||||||  
 Db 1506 agccggcgcatctatgtcttccaggtgcggacacgcgtgacaggtcagcagcagcagccta 1565  
 QY 1509 CACGCGCAAGATGATCTTACATGACGACATGACAGAGCGGAGTATCAGCAAGATCCAGGA 1568  
 |||||||  
 Db 1566 cagcgcaagatgttacttccagacccatgacagagccgatataccagcaagcttccagga 1625  
 QY 1569 GAAGTTCACATCATATGCGCTCTCGGCGCGCTGGCTGTGCTTCTCATTTGCTGTGT 1628  
 |||||||  
 Db 1626 gaagtgtcacatcatcatctgcgtccctcgccgtgtgctgtctctcatctgtgtgt 1685  
 QY 1629 TGTGATCGCATGCTGTGTGAACAGAGGGGGGTTTGAAGCTGTGACTCGGAGTACACGGA 1688  
 |||||||  
 Db 1686 tgcatacgcacatctgtgttaacagacgaggggttltgagctgtcagctcagagctacagga 1745  
 QY 1689 CAAGTGCACACTACACAGTGGCCACATTAACCCAGGATGATGATCATCTCATCTGATCC 1748  
 |||||||  
 Db 1746 caagctgcaaacactataccagtggtgccaatgaccccaagcatgaaatctacatctcc 1805  
 QY 1749 TTTACCTTACGAGAGCCCAACGAGGACAGTGCGGAGTTGCCAAGAAATTGACATCTC 1808  
 |||||||  
 Db 1806 ttccactcagagagcaccacagagcagtgcgaggtlttgccaagaaattgacatctc 1865  
 QY 1809 CTGTGTCAAAATTTGAGCAGGTATCGGAGGAGGTTTGGGAGGCTGTGCAAGTGGCCA 1868  
 |||||||  
 Db 1866 cgtgtgcaaaatltgacagagtgatcgagcagggaggtlttgagaggtltgacagtggtgca 1925  
 QY 1869 CCTGAAGCTCCAGGAGAGAGAGATCTTTGTGGCCATCAAGACGCTCAAGTCGGGCTA 1928  
 |||||||  
 Db 1926 cctgaagctcgccagagagagagatcttltgtgccaataagacagctaaagtctgggtcta 1985  
 QY 1929 CACGGAGAAAGCAGCGCGGAGCTTCTGAGCAAGCCTTCATCANGGCGCAGTTGACCA 1988  
 |||||||  
 Db 1986 cagggagagagcagcgccgagacttctgtgagcagcctcatcaltgagcagltcgacca 2045  
 QY 1989 TCCCAAGCTCATCAACCTTGAGAGGTGCTGTGACCAAGACACACCTGTATATCATCTAC 2048  
 |||||||  
 Db 2046 tcccaacgctacacccacccgtgaggtgtgtgtgaccaagacacacccgtgtatgatactac 2105  
 QY 2049 CGAGTTTCATGGAATGCGTCCCTGACTCTTTCTCCGGCAAAAGATGGCGCAGTTTAC 2108  
 |||||||  
 Db 2106 cgagttcatgagagatgtgtccctgtaccttcttcggaacagatggtgcaagttcac 2165

QY 2109 AGTATCCACACTGTGTGGGACATGCTTCGGGCGATCGAGCTGGCATGATACCTGGCAGA 2168  
 |||||||  
 Db 2166 agtcatccagctgtgtgtgcatgtcttgcgggcatcgcagcgtcgatgaagtaactcgtcgaga 2225  
 QY 2169 CATGAATATGTTTCAACGCTACCTGGCTGCGCCGCAACATCTCTGTCAACAGCAACTGGT 2228  
 |||||||  
 Db 2226 catgaactatgtttcacccgtgacacgtgtgctgcgcgaacatctcgtcaacagcaactgtt 2285  
 QY 2229 CTGCAAGGTGTGGAGCTTTGAGGCTTCACGCTTTTGAAGAGAGATACCTCAACCCAC 2288  
 |||||||  
 Db 2286 ctgcaaggtgtggtcttgtggtcttcaagcttctcagaagacatacccaagcccaac 2345  
 QY 2289 CTACACCAATGTCCTGTGGCGGAAAGTTCCCATCCGCTGTGACAGCCCGGAAACCATCA 2348  
 |||||||  
 Db 2346 ctacacacagtgcccttggcggaagatccccatccgcttgacagcccccggaagcattca 2405  
 QY 2349 GTACCGGAAGTTACCTCGGCGCATGATGTGTGAGCTTACGGCATTTGTATGTGGAGGT 2408  
 |||||||  
 Db 2406 gtaccggaagttcacctcgtgcagtgatgtgtgagctacgcagctatgtcatgtggaagt 2465  
 QY 2409 GATGTCTATGGGGAGCGGCGCTACTGGGACATGACCAACGAGATGTATCAATGCCAT 2468  
 |||||||  
 Db 2466 gatgtctatggtggtgagcgccctacatggtgacatgacacacaggaatgataatgcat 2525  
 QY 2469 TGAAGAGACTATCGGCTGCGACCGCCCATGAGTGCAGGAGCGCCCTGCACCAACTCAT 2528  
 |||||||  
 Db 2526 tggagagagctatcgtgtgcacccgcacatgtgactgtccagctgccttcgacacatcat 2585  
 QY 2529 GCTGAGCTGTGGCAAGAGACCGCAACACCGGCCCAAGTTGCGCAAAATTGTCAACAC 2588  
 |||||||  
 Db 2586 gctgagactgttgcagaagagacgcgcaacacacgcagcttgcgcaaatgttcaaacac 2645  
 QY 2589 GCTAGCAAGATGATCCGGAATCCCAACAGCCCTCAAGGCGATGGCGCCCTGCTCTGTG 2648  
 |||||||  
 Db 2646 gctagcaagaatgatctgcgaatcccaacacagcctcaagcagatggtgccccctctcgtg 2705  
 QY 2649 CATCAACTGCGCGCTCTGTGAGCGCACGATGCCCGACTACACAGCTTTTACACGGTGA 2708  
 |||||||  
 Db 2706 catcaacccgtcgtgtgtgacgcagacagatccccgcgtacacagtttaacaacgttga 2765  
 QY 2709 CGAGTGGCTGGAAGCCATTAAGTGGGCGAGTACAAAGAGAGCTTGGCAATGCCGCTT 2768  
 |||||||  
 Db 2766 cgagtgtcgtgaagccatcaaatggtgagcagtaagaagagcttgcgaatgtccggtct 2825  
 QY 2769 CACCTCTTTGAGAGTGTGTCATGATGATGATGAGGACATTTCCGGGTTGGGGTCA 2828  
 |||||||  
 Db 2826 cactctcttgaagctgtgtccagatgatgatgagagacattcccggttctggtgtcac 2885  
 QY 2829 TTTGGCTGCGCACAGAAAAAATCCTGAACAGTATCCAGTGTATGCGGCGCAGATGA 2888  
 |||||||  
 Db 2886 ttgtgtgtgcacacaggaaaaaatccctgaaacagatccagtgatgtggtgagatgaa 2945  
 QY 2889 CCAGATTCAGTGTGTGAGAGTTTGAATTCACCTGCTGTGCTCACCTTCTTCCAGC 2948  
 |||||||  
 Db 2946 ccagatltcagctgtgtgaggtlttgacatcacctgtcctgtcaccctcttcccaagc 3005  
 QY 2949 CCGGCCCTCTGC 2962  
 |||||||  
 Db 3006 cccgcccctctgc 3019

RESULT 5  
 AA096250  
 ID AA096250 standard; cDNA to mRNA; 171 BP.  
 XX  
 AC AA096250;  
 XX  
 DT 22-FEB-1996 (first entry)  
 XX  
 DE Partial DNA encoding human receptor type kinase.  
 XX receptor type kinase; osteoblast; screening; anti-cancer; diagnosis;  
 KM treatment; bone disease; ds.

XX Homo sapiens.  
 OS JF07155187-A.  
 PN 20-JUN-1995.  
 PD 03-DEC-1993; 93JP-0303622.  
 PF 03-DEC-1993; 93JP-0303622.  
 PR 03-DEC-1993; 93JP-0303622.  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 PA WPI: 1995-250736/73.  
 DR P-PSDB; AAR79141.  
 XX Human receptor type tyrosine kinase partial cDNA - used to develop  
 PT medications for the treatment of bone disease caused by  
 PT proliferation of osteoblast cells  
 PS Claim 1; Page 5; 5pp; Japanese.  
 CC The DNA encodes a human receptor type tyrosine kinase isolated from a  
 CC human osteoblastoid cell line (MG63) by reverse transcriptase-polymerase  
 CC chain reaction. The gene fragment can be used for the screening of  
 CC cells for anti-cancer agents, and for treatment of bone diseases due to  
 CC the proliferation of osteoblasts.  
 SQ Sequence 171 BP; 39 A; 60 C; 41 G; 31 T; 0 other;

Query Match 4.1%; Score 120; DB 16; Length 171;  
 Best Local Similarity 99.4%; Pred. No. 9.2e-49;  
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2203 AACATCCTCTGTCACACCACTGCTGTCTGCAAGTGTGCGACTTTGGCTCTCAGCTTT 2262  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 AACATCCTCTGTCACACCACTGCTGTCTGCAAGTGTGCGACTTTGGCTCTCAGCTTT 60  
 OY 2263 CTAGAGGAGCATATCTCAGACCCCACTACACCACTGCTGTGCGGCGAAGTTCCCAATC 2322  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 CTAGAGGAGCATATCTCAGACCCCACTACACCACTGCTGTGCGGCGAAGTTCCCAATC 120  
 OY 2323 CGCTGGACAGCCCCGGAGACCATCCAGTACCGGAAGTTCACTCGGCCAGT 2373  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CGCTGGAGAGCCCCGGAGAGCATCCAGTACCGGAAGTTCACTCGGCCAGT 171

RESULT 6  
 AA060025  
 ID AA060025 standard; cDNA; 381 BP.  
 AC AA060025;  
 XX 16-MAR-1994 (first entry)  
 DT Human Brain Expressed Sequence Tag EST02007.  
 DE  
 XX Gene transcription product; genetic markers; tagging; in vivo;  
 KM transcription; mapping; locations; chromosomes; chromosomal; ss.  
 OS Homo sapiens.  
 PN WO9316178-A.  
 PD 19-AUG-1993.  
 PF 12-FEB-1994; 94WO-US01294.  
 PR 12-FEB-1994; 94US-0837195.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX

PI Adams MD, Moreno RF, Venter CJ;  
 DR WPI: 1993-272882/34.  
 XX Enriched oligonucleotides and corresp. sequences - used as  
 PT markers for human genes transcribed in-vivo, facilitate tagging  
 PT of most human genes  
 PS Example 4; Page 269; 500pp; English.  
 CC The Expressed Sequence Tag was isolated from a human brain cDNA  
 CC library as part of a large set of ESTs which can be used as markers  
 CC for human genes transcribed in vivo. They can be used to facilitate  
 CC tagging of most human genes, for mapping locations of expressed genes  
 CC on chromosomes, for individual or forensic identification, for mapping  
 CC locations of disease-associated genes, for identification of tissue  
 CC type, and for prepn. of antisense sequences, probes and constructs.  
 CC EST02007 has been putatively identified as encoding a kinase 5  
 CC protein. See also AA055041-061440.  
 SQ Sequence 381 BP; 91 A; 100 C; 110 G; 75 T; 5 other;

Query Match 2.9%; Score 85; DB 14; Length 381;  
 Best Local Similarity 98.9%; Pred. No. 1.3e-31;  
 Matches 185; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1778 TGGCGAGTTGCCAAGAAATTGACATCTCTGTGCAAAATTGACGAGTGTGCGAG 1837  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 35 TGGCGAGTTGCCAAGAAATTGACATCTCTGTGCAAAATTGACGAGTGTGCGAG 94  
 OY 1838 CAGGCGAGTTGGCGAGTCTGCACTGGCCACCTTAAGCTGCCAGCAAGAGAGATCT 1897  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 95 CAGGCGAGTTGGCGAGTCTGCACTGGCCACCTTAAGCTGCCAGCAAGAGAGATCT 154  
 OY 1898 TTGTGGCATCAAGAGCGTCAAGTGGGCTACACGAGAGAGCGCGGACTTCTGA 1957  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 155 TTGTGGCATCAAGAGCGTCAAGTGGGCTACACGAGAGAGCGCGGACTTCTGA 214  
 OY 1958 GCGAAGC 1964  
 ||||||||  
 Db 215 GCGAAGC 221

RESULT 7  
 AA07308  
 ID AA07308 standard; cDNA; 3105 BP.  
 AC AA07308;  
 XX 19-MAR-1996 (first entry)  
 DT Receptor tyrosine kinase (neural kinase) cDNA.  
 DE Receptor tyrosine kinase (neural kinase) cDNA.  
 XX Receptor tyrosine kinase; neural kinase; Nuk gene; axon;  
 KM axonogenesis; nerve disorder; gene therapy; transgenic animal; ss.  
 OS Mus musculus.  
 PN  
 FT Key Location/Qualifiers  
 FT CDS 1..2985  
 FT sig\_peptide /\*tag= a  
 FT mat\_peptide /\*tag= b  
 FT /\*tag= 79..2982  
 FT /\*tag= c  
 PN WO9530326-A1.  
 PD 09-NOV-1995.  
 PR 28-APR-1995; 95WO-CA00254.  
 PF  
 XX

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PR 29-APR-1994; 94US-0235407.
XX
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX
XX Henkemeyer M, Letwin K, Pawsan A;
XX
XX WPI; 1995-393299/50.
XX
XX P-PSDB; AAR87018.
XX
XX DNA encoding neural receptor tyrosine kinase - useful in gene
XX therapy of nerve disorders, and for diagnosis and identification of
XX therapeutic agents
XX
XX Claim 2; Page 68-70; 103pp; English.
XX
XX CC CDNA clones pNURACE A2 and K2 were combined to obtain a sequence
XX CC (AAT07308) coding for a novel receptor tyrosine kinase, designated
XX CC neural kinase (Nuk) (AAR87018). The clones were obtd. from a CDNA
XX CC library of mouse embryo CDNA in lambda-gt10 probed with a partial Nuk
XX CC CDNA insert. The gene was mapped to the distal end of chromosome 4
XX CC near the abd-1 mutation. The CDNA is used to produce recombinant
XX CC Nuk or transgenic animal models for studies of Nuk function, or as
XX CC probes to detect genes or diagnose conditions associated with Nuk
XX CC gene mutation, or in gene (antisense) therapy of disorders of the
XX CC nervous system.
XX
XX SQ Sequence 3105 BP; 711 A; 937 C; 847 G; 610 T; 0 other;

Query Match
Best Local Similarity 1.6%; Score 48; DB 16; Length 3105;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1440 GGGCGTCAAGCCGGCGCATCTATGCTTCCAGGTCGGGACCGCAC 1487
    |||||||||||||||||||||||||||||||||||||||||||
Db 1512 gggccctaaagccggcgccatctatgtctccaggtcgggcagcgac 1559

RESULT 8
AAT84528
ID AAT84528 standard; cDNA; 3105 BP.
XX
XX AAT84528;
XX
XX 02-DEC-1997 (first entry)
XX
XX Mouse Nuk tyrosine kinase cDNA.
XX
XX Nuk tyrosine kinase; Eph receptor tyrosine kinase;
XX KW signal transduction; axonogenesis; neurodegenerative disease;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX KW multiple sclerosis; amyotrophic lateral sclerosis;
XX KW Wernicke's disease; nerve damage; trauma; ischaemia; stroke; ss.
XX
XX Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT 1..2985
XX FT sig_peptide /tag= a
XX FT 1..78
XX FT mat_peptide /tag= b
XX FT 79..2982
XX FT /tag= c
XX
XX WO9714966-A1.
XX
XX PD 24-APR-1997.
XX
XX PF 10-OCT-1996; 96WO-CA00679.
XX
XX PR 13-OCT-1995; 95US-0005518.
XX
XX PA (MOUN ) MOUNT SINAI HOSPITAL CORP.

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XX
XX Henkemeyer M, Pawsan A;
XX
XX WPI; 1997-245245/22.
XX
XX P-PSDB; AAW26366.
XX
XX PT Activation of ligand regulatory pathways by Eph subfamily receptor
XX PT tyrosine kinases - for stimulating or inhibiting axonogenesis,
XX PT useful for treatment of e.g. neurodegenerative diseases such as
XX PT Alzheimer's or Parkinson's diseases
XX
XX PS Disclosure; Page 24-25; 55pp; English.
XX
XX CC This CDNA sequence codes for murine Nuk tyrosine kinase (AAW26366),
XX CC an Eph subfamily receptor tyrosine kinase essential for formation
XX CC of the medial tract of the anterior commissure of the brain. Its
XX CC sequence was deduced from clones isolated from an embryo CDNA
XX CC library in lambda gt10. The Nuk gene maps to the distal end of
XX CC chromosome 4 near the abd-1 mutation. Eph subfamily receptor
XX CC tyrosine kinases (e.g. Nuk extracellular domain polypeptides)
XX CC can be used in claimed methods to: activate a ligand regulatory
XX CC pathway in a cell; identify a substance able to bind a ligand for
XX CC an Eph subfamily receptor tyrosine kinase; and to affect neuronal
XX CC development or regeneration, especially the stimulation or
XX CC inhibition of axonogenesis, in a mammal. Activation of the ligand
XX CC regulatory pathway results in downstream activation of a series of
XX CC regulatory pathways in cells that control gene expression, cell
XX CC division, cytoskeletal architecture, cell metabolism, cell
XX CC migration and cell-cell interactions. Substances which activate
XX CC the ligand regulatory pathway may be used for stimulating or
XX CC inhibiting neuronal development, regeneration and axonal migration
XX CC associated with neurodegenerative disease e.g. Alzheimer's,
XX CC Parkinson's or Huntington's diseases, multiple sclerosis,
XX CC amyotrophic lateral sclerosis, deficiency diseases such as
XX CC Wernicke's disease, peripheral nerve damage, trauma and ischaemia
XX CC resulting from stroke.
XX
XX SQ Sequence 3105 BP; 710 A; 937 C; 848 G; 610 T; 0 other;

Query Match
Best Local Similarity 1.6%; Score 48; DB 18; Length 3105;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1440 GGGCGTCAAGCCGGCGCATCTATGCTTCCAGGTCGGGACCGCAC 1487
    |||||||||||||||||||||||||||||||||||||||||||
Db 1512 gggccctaaagccggcgccatctatgtctccaggtcgggcagcgac 1559

RESULT 9
AAQ90655
ID AAQ90655 standard; cDNA; 3776 BP.
XX
XX AAQ90655;
XX
XX 11-NOV-1995 (first entry)
XX
XX Eph-related PTK Cdk5 cDNA.
XX
XX KW Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
XX KW prognosis; ss.
XX
XX OS Gallus sp.
XX
XX FH Key Location/Qualifiers
XX FT 290..3311
XX FT /tag= a
XX
XX WO9515375-A.
XX
XX PD 08-JUN-1995.
XX
XX PF 07-SEP-1994; 94WO-US10140.

```

XX 03-DEC-1993; 93US-0162809.  
XX (JOL-) LA JOLLA CANCER RES FOUND.  
XX  
XX Pasquale EB, Sajjadi FG;  
XX  
XX WPI: 1995-215256/28.  
XX P-PSDB: AAR75707.  
XX  
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
XX cancer.  
XX  
XX Claim 2; Page 50-53; 129pp; English.  
XX  
XX Novel Eph-related PTK cDNA clone Cek9 (given in AAQ90655) was  
XX isolated from a chick embryo library in lambda. Cek9 protein  
XX (AAR75707) is closely related to Cek5 (AAR75712). In adult tissues,  
XX Cek9 expression is predominant in the thymus and detectable in  
XX brain, retina, kidney, lung and heart.  
XX  
XX Sequence 3776 BP; 1005 A; 881 C; 941 G; 949 T; 0 other;

Query Match 1.1%; Score 32; DB 16; Length 3776;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2389 GGCATGTCATGCGAGCGATGCTCCATGG 2420  
DB 2687 ggcattgcatcgtggaagtgatgctcctatg 2718

RESULT 10  
AAQ62461  
ID AAQ62461 standard; cDNA: 3751 BP.  
XX  
XX AAQ62461;  
XX  
XX 09-NOV-1994 (first entry)  
XX  
XX Human embryonal kinase 2 receptor.  
XX  
XX Embryonal kinase; HEK; protein tyrosine kinase; PTK; tumour;  
XX cancer; therapy; amplification; primer; polymerase chain reaction;  
XX PCR; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT 1..2973  
XX CDS /\*tag= a  
XX  
XX DE4233782-A.  
XX  
XX 14-APR-1994.  
XX  
XX 07-OCT-1992; 92DE-4233782.  
XX  
XX 07-OCT-1992; 92DE-4233782.  
XX  
XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.  
XX  
XX Holtrich U, Ruebsamen-Waigmann H, Strebhardt K;  
XX  
XX WPI: 1994-127194/16.  
XX P-PSDB: AAR51899.  
XX  
XX Human embryonal kinase 2-receptor protein - useful in tumour  
XX diagnosis and therapy  
XX  
XX Claim 4; Page 7-10; 11pp; German.  
XX

CC RNA from human embryonic tissue was isolated. With the use of  
CC primer P6(4) PTK-specific cDNA was synthesised. The cDNA was  
CC amplified using primers P6(4) and N5. A 2097 bp DNA fragment was  
CC obtained. Primers E3, P12 and E6 were then used in the isolation of  
CC the C-terminal of the HEK2 receptor gene.  
XX  
XX Sequence 3751 BP; 739 A; 1150 C; 1123 G; 739 T; 0 other;

Query Match 1.0%; Score 30; DB 15; Length 3751;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 GGTGGGAGAGGTGAGTGTACGATGAG 111  
DB 157 ggcgcggaagagcgtgagtgctacgatgag 186

RESULT 11  
AAQ90652  
ID AAQ90652 standard; cDNA: 3133 BP.  
XX  
XX AAQ90652;  
XX  
XX 11-NOV-1995 (first entry)  
XX  
XX Eph-related tyrosine kinase CEK6 cDNA.  
XX  
XX CEK6; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
XX prognosis; ss.  
XX  
XX Gallus sp.  
XX  
XX Key Location/Qualifiers  
XX FT 3..419  
XX CDS /\*tag= a  
XX FT 421..2859  
XX CDS /\*tag= b

XX  
XX W09515375-A.  
XX  
XX 08-JUN-1995.  
XX  
XX 07-SEP-1994; 94WO-US10140.  
XX  
XX 03-DEC-1993; 93US-0162809.  
XX  
XX (JOL-) LA JOLLA CANCER RES FOUND.  
XX  
XX Pasquale EB, Sajjadi FG;  
XX  
XX WPI: 1995-215256/28.  
XX P-PSDB: AAR75704.  
XX  
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
XX cancer.  
XX  
XX Disclosure: Page 37-41; 129pp; English.  
XX  
XX Novel Eph-related PTK Cek6 cDNA clones (AAQ90652) were isolated from  
XX chick embryo and embryonic brain cDNA libraries in phage lambda gtl1.  
XX The encoded Cek6 protein (AAR75704) is closely related to rat Elk,  
XX Cek5 (AAR75712) and Cek10 (AAR75708). Cek6 transcripts were found in  
XX 10-day embryos and in adult brain, lung, heart and skeletal muscle.  
XX  
XX Sequence 3133 BP; 718 A; 918 C; 922 G; 575 T; 0 other;

Query Match 1.0%; Score 29; DB 16; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 271 GGCCTCTGCAAGAGACCTTCAACCTTA 299

Db 255 ggcctcgcgaagagacctcaacctcta 283  
 |||

## RESULT 12

AAV70208  
 ID AAV70208 standard; DNA; 3592 BP.

AC AAV70208;

DT 11-FEB-1999 (first entry)

DE Rat receptor tyrosine kinase Etk-2 encoding DNA.

KM Receptor tyrosine kinase; Ror-1; Ror-2; Etk-1; Etk-2; detection;

KM neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;

OS binding protein; BDNF; NR-3; diagnosis; ss.

XX Rattus sp.

XX Key Location/Qualifiers

XX CDS 598..3444

XX FT /\*tag= a

XX US5843749-A.

XX 01-DEC-1998.

XX 06-JUN-1995; 95US-0469537.

XX 17-MAR-1995; 95US-0406247.

XX 26-JUL-1991; 91US-0736559.

XX 28-OCT-1993; 93US-0144992.

XX 06-JUN-1995; 95US-0469537.

XX (REGF-) REGENERON PHARM INC.

XX Maisompierre PC, Maslakowski P, Yancopoulos GD;

XX WPI; 1999-044584/04.

XX P-PSDB; AAW83148.

XX DNA encoding receptor tyrosine kinase proteins - and corresponding

XX proteins

XX Claim 7; Fig 21; 194pp; English.

XX The present invention describes nucleic acid molecules for ror-1,

XX ror-2, etk-1 and etk-2. Also described are the corresponding proteins:

XX Ror-1; Ror-2; Etk-1; and Etk-2. The proteins are orphan receptor

XX tyrosine kinases. The present sequence encodes rat Etk-2.

XX Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T; 2 other;

XX Query Match 1.0%; Score 29; DB 20; Length 3592;

XX Best Local Similarity 100.0%; Pred. No. 0.00035;

XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2392 ATGTGATGAGGAGGATGCTGCTATGG 2420

XX 3184 atgtcactgtggaagtgatgtctatgg 3212.

## RESULT 13

AAQ90660  
 ID AAQ90660 standard; DNA; 4049 BP.

AC AAQ90660;

DT 11-NOV-1995 (first entry)

DE Eph-related PTK Cdk5.

XX Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

XX prognosis; ss.

XX Gallus sp.

XX Key Location/Qualifiers

XX CDS 10..2997

XX FT /\*tag= a

XX WO9515375-A.

XX 08-JUN-1995.

XX 07-SEP-1994; 94WO-US10140.

XX 03-DEC-1993; 93US-0162809.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Pasquale EB, Sajjadi FG;

XX WPI; 1995-215256/28.

XX P-PSDB; AAR75712.

XX EPH-related protein tyrosine kinase(s) - for monitoring and diagnosing

XX cancer.

XX Disclosure; Page 92-96; 129pp; English.

XX Probes derived from the EPH-related PTKs Cdk4 (AAQ90659) and Cdk5

XX (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58,

XX AAQ90661-62) from chicken embryo and embryonic brain libraries.

XX Sequence 4049 BP; 1010 A; 1011 C; 1072 G; 956 T; 0 other;

XX Query Match 1.0%; Score 29; DB 16; Length 4049;

XX Best Local Similarity 100.0%; Pred. No. 0.00035;

XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2212 GTCAACAGCAACCTGCTGCAAGGTGTC 2240

XX 2296 gtcaacagcaacctgtctgcaaggtgtc 2324

XX RESULT 14

XX AAQ90657

XX ID AAQ90657 standard; DNA; 4097 BP.

XX AC AAQ90657;

XX 11-NOV-1995 (first entry)

XX Eph-related PTK Cdk5+.

XX Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

XX prognosis; ss.

XX Gallus sp.

XX Key Location/Qualifiers

XX CDS 10..3045

XX FT /\*tag= a

XX WO9515375-A.

XX 08-JUN-1995.

XX 07-SEP-1994; 94WO-US10140.

XX 03-DEC-1993; 93US-0162809.



PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Pasquale EB, Sajjadi FG;  
 XX  
 DR WPI; 1995-215256/28.  
 DR P-PSDB; AAR75709.  
 XX  
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 PT cancer.  
 PS  
 PS Claim 2; Page 71-75; 129pp; English.  
 XX  
 CC A cDNA clone encoding a novel variant of EPH-related PTK Cdk5,  
 CC Cdk5+ (AA090657), was isolated from a chick embryo library in  
 CC lambda gt11. Cdk5+ protein (AAR75709) contains a 16-amino acid  
 CC insertion in the juxtamembrane domain, and be a result of  
 CC alternative splicing. Cdk5+ is exclusively expressed in the CNS.  
 CC  
 XX  
 SQ Sequence 4097 BP; 1014 A; 1029 C; 1087 G; 967 T; 0 other;

Query Match 1.0%; Score 29; DB 16; Length 4097;  
 Best Local Similarity 100.0%; Pred. No. 0.00035;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2212 GTCACAGCAGCAGCTGCTGCAGAGTGC 2240  
 ||||||||||||||||||||||||||||  
 DB 2344 gtcaacagcaacctgctgtcgaagtgtc 2372

## RESULT 15

AA053470  
 ID AA053470 standard; DNA; 1509 BP.

AC AA053470;

DT 16-JUN-1994 (first entry)

DE PTK gene B1.

XX  
 KW Lambda gt11; expression vector: lambda-B1-Elk; protein tyrosine kinase:  
 KW Elk; B1; Eph; subfamily; receptor-like tyrosine kinase; eph; eck;  
 KW phosphorylation; phosphorylated kinase insert domain; growth factor;  
 KW receptor kinase; platelet-derived growth factor receptor; ss.

OS Rattus rattus.

XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1143  
 FT /\*tag= a  
 FT /product= Elk

PN CA2083521-A.

PD 01-OCT-1993.

PF 23-NOV-1992; 92CA-2083521.

PR 31-MAR-1992; 92US-0861390.

XX (MOUN ) MOUNT SINAI HOSPITAL CORP.

PI Letwin K, Pawson A, Reedijk M;

DR WPI; 1993-406300/51.

DR P-PSDB; AAR44512.

XX  
 PT Expression of phosphorylated exogenous protein - in host cells  
 PT transformed with two vectors, one for the protein, the other for  
 PT catalytic domain of protein kinase

PS Disclosure: Fig 1; 55pp; English.  
 XX

CC This sequence represents a fragment of the lambda gt11 expression  
 CC vector, lambda-B1-Elk, which encodes the catalytic sequence of the  
 CC protein tyrosine kinase, Elk. The Elk gene, B1, encodes a protein  
 CC which is a member of the Eph subfamily of protein tyrosine kinases.  
 CC The Elk product is very similar to two other receptor-like tyrosine  
 CC kinases, eph and eck. Lambda-B1-Elk may be used in the production  
 CC of phosphorylated exogenous protein along with a further vector  
 CC encoding the desired exogenous protein. These plasmid may be used  
 CC to produce phosphorylated proteins in host cells which have no  
 CC intrinsic capacity for phosphorylation, eg. bacteria. The system  
 CC may be used for the expression of the phosphorylated kinase insert  
 CC domain of a growth factor receptor kinase eg. platelet-derived growth  
 CC factor receptor.  
 CC  
 XX  
 SQ Sequence 1509 BP; 393 A; 374 C; 429 G; 313 T; 0 other;

Query Match 0.9%; Score 26; DB 14; Length 1509;  
 Best Local Similarity 100.0%; Pred. No. 0.01;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2524 CTCATGCTGACACTGTGACAGAGA 2549  
 ||||||||||||||||||||||||  
 DB 754 ctcatgctgacctgttgacagaaga 779

Search completed: July 10, 2001, 21:22:37  
 Job time: 9649 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 18:40:58 ; Search time 88.1 seconds  
(without alignments)  
6228.617 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CTGCTCGCCGCCGTGGAAGA.....CCAGCCCGCCCTCTGC 2962

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Capext 60.0

Searched: 317530 seqs, 92630169 residues

Word size: 0

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued\_Patents\_NA: \*  
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3: /cgn2\_6/ptodata/2/1na/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/1na/PCNUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/1na/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2962	100.0	2962	2	US-08-449-645A-10 Sequence 10, Appl
2	2962	100.0	2962	2	US-08-702-367A-10 Sequence 10, Appl
3	2962	100.0	2962	5	PCT-US95-04681-10 Sequence 10, Appl
4	48	1.6	3105	4	US-08-542-635-1 Sequence 1, Appl
5	35	1.2	162	2	US-08-469-537A-28 Sequence 28, Appl
6	32	1.1	3776	1	US-08-162-809-7 Sequence 7, Appl
7	29	1.0	3133	1	US-08-162-809-1 Sequence 1, Appl
8	29	1.0	3592	2	US-08-469-537A-100 Sequence 100, App
9	29	1.0	4049	1	US-08-162-809-17 Sequence 17, Appl
10	29	1.0	4097	1	US-08-162-809-11 Sequence 11, Appl
11	25	0.8	39	2	US-08-449-645A-23 Sequence 23, Appl
12	25	0.8	39	2	US-08-702-367A-23 Sequence 23, Appl
13	25	0.8	39	5	PCT-US95-04681-23 Sequence 23, Appl
14	25	0.8	81	2	US-08-469-537A-65 Sequence 65, Appl
15	25	0.8	3546	1	US-08-162-809-9 Sequence 9, Appl
16	25	0.8	3591	1	US-08-162-809-13 Sequence 13, Appl
17	25	0.8	24	2	US-08-449-645A-22 Sequence 22, Appl
18	24	0.8	24	2	US-08-702-367A-22 Sequence 22, Appl
19	24	0.8	24	5	PCT-US95-04681-22 Sequence 22, Appl
20	24	0.8	54	2	US-08-449-645A-25 Sequence 25, Appl
21	24	0.8	54	2	US-08-702-367A-25 Sequence 25, Appl
22	24	0.8	54	5	PCT-US95-04681-25 Sequence 25, Appl
23	24	0.8	3969	1	US-08-436-044-5 Sequence 5, Appl
24	24	0.8	3969	1	US-08-222-616-23 Sequence 23, Appl
25	24	0.8	3969	2	US-08-436-054-5 Sequence 5, Appl
26	24	0.8	3969	5	PCT-US95-04228-23 Sequence 23, Appl
27	24	0.8	3969	5	PCT-US95-08812-5 Sequence 5, Appl

28	23	0.8	171	1	US-08-456-647B-9	Sequence 9, Appl
29	23	0.8	171	2	US-08-237-401A-9	Sequence 9, Appl
30	23	0.8	2982	1	US-08-348-143-2	Sequence 2, Appl
31	23	0.8	2982	1	US-08-571-785-2	Sequence 2, Appl
32	23	0.8	3056	1	US-08-162-809-21	Sequence 21, Appl
33	23	0.8	3059	1	US-08-162-809-3	Sequence 3, Appl
34	23	0.8	3125	1	US-08-162-809-19	Sequence 19, Appl
35	23	0.8	4027	1	US-08-348-143-3	Sequence 3, Appl
36	23	0.8	4027	1	US-08-348-143-4	Sequence 4, Appl
37	23	0.8	4027	1	US-08-571-785-3	Sequence 3, Appl
38	23	0.8	4027	1	US-08-571-785-4	Sequence 4, Appl
39	22	0.7	171	1	US-08-456-647B-11	Sequence 11, Appl
40	22	0.7	171	2	US-08-237-401A-11	Sequence 11, Appl
41	21	0.7	3162	2	US-08-449-645A-12	Sequence 12, Appl
42	21	0.7	3162	2	US-08-702-367A-12	Sequence 12, Appl
43	21	0.7	3162	5	PCT-US95-04681-12	Sequence 12, Appl
44	20	0.7	171	1	US-08-456-647B-21	Sequence 21, Appl
45	20	0.7	171	2	US-08-237-401A-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-08-449-645A-10  
; Sequence 10, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,645A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2962 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2913  
; US-08-449-645A-10

Query Match 100.0%; Score 2962; DB 2; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCGCCGCCGTGGAAGAAAGCTATGAGCTCCTACAGCGAGCTGAGCTGGGC 60  
DB 1 CTGCTCGCCGCCGTGGAAGAAAGCTATGAGCTCCTACAGCGAGCTGAGCTGGGC 60  
QY 61 TGGATGTCATCTCCATCAGAGGTGGAAGAGTGAAGTGGCTACAGATGAGAAATGAAC 120

|||||  
Db 61 TGAATGATGATCTCCATCATGAGGGGAGAGAGGTGATGGCTACGATGAGATGATGAC 120  
QY 121 AGCATCCGACATACGACAGGTGCAAGCTGTTAGTCAAGCCGAAACACTGGCTACGG 180  
Db 121 AGCATCCGACATACGACAGGTGCAAGCTGTTAGTCAAGCCGAAACACTGGCTACGG 180  
QY 181 ACCAAGTTTATCCGGCCCGCTGGGGCCACCGCATCCACGATGAGATGAAGTTTTCGGTG 240  
Db 181 ACCAAGTTTATCCGGCCCGCTGGGGCCACCGCATCCACGATGAGATGAAGTTTTCGGTG 240  
QY 241 CGTACTGACAGCAGATCCCGAGCGTGTGCTCTGCAAGAGAGACTTCAACCTCTAT 300  
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Db 301 TACTATGAGGCTGACTTGTGATGCTGGCCACCAAGACTTCCCAACTGATGAGAAATCCA 360  
QY 361 TGGGTGAAGGTGATATACATTTGACGCGAGAGAGCTTCCCGAGGTGAGCTGGTGGC 420  
Db 361 TGGGTGAAGGTGATATACATTTGACGCGAGAGAGCTTCCCGAGGTGAGCTGGTGGC 420  
QY 421 CGGCTATGAAAATCAACACCGAGGTGCGAGCTTCGAGCTGTGTCCGACGCGCTTC 480  
Db 421 CGGCTATGAAAATCAACACCGAGGTGCGAGCTTCGAGCTGTGTCCGACGCGCTTC 480  
QY 481 TACTGGCCCTTCCAGAGCTATGCGGCTGATGTCTCATCCGCGTGTCTTCTAC 540  
Db 481 TACTGGCCCTTCCAGAGCTATGCGGCTGATGTCTCATCCGCGTGTCTTCTAC 540  
QY 541 CGCAAGTGGCCCGCATCATCCAGAAATGCGCCATCTTCCAGAAACCTGTGGGGGCT 600  
Db 541 CGCAAGTGGCCCGCATCATCCAGAAATGCGCCATCTTCCAGAAACCTGTGGGGGCT 600  
QY 601 GAAAGCATATCGCTGTGTGCTGCCCGGGGCACTGATCGCAATGCGAAGAGGTGAT 660  
Db 601 GAAAGCATATCGCTGTGTGCTGCCCGGGGCACTGATCGCAATGCGAAGAGGTGAT 660  
QY 661 GTACCCATCAAGCTTACTGTAAAGGGGAGGAGGTGTGTGCTCCATCGGGGCTGC 720  
Db 661 GTACCCATCAAGCTTACTGTAAAGGGGAGGAGGTGTGTGCTCCATCGGGGCTGC 720  
QY 721 ATGTGAAAACGAGCTTGCAGGCGTTGAGAAATGAGCACTGTGCGAGGTTTTCATCT 780  
Db 721 ATGTGAAAACGAGCTTGCAGGCGTTGAGAAATGAGCACTGTGCGAGGTTTTCATCT 780  
QY 781 GGGACTTTCAAGGCCAACAAGGGGATGAGGCTGTACCCACTGTCCATCAACACCGG 840  
Db 781 GGGACTTTCAAGGCCAACAAGGGGATGAGGCTGTACCCACTGTCCATCAACACCGG 840  
QY 841 ACCACTTTGAAAGGGGCAACCACTGTGTGCGCAATGAGTACTACAGAGAGACTG 900  
Db 841 ACCACTTTGAAAGGGGCAACCACTGTGTGCGCAATGAGTACTACAGAGAGACTG 900  
QY 901 GACCCCTTGACATGCTGTGCAACACCATCCCTCGCGCCCGAGGCTGTGATTTCCAGT 960  
Db 901 GACCCCTTGACATGCTGTGCAACACCATCCCTCGCGCCCGAGGCTGTGATTTCCAGT 960  
QY 961 GTCAATGAGACCTCCCTCAATGCTGAGTGGAGTGGACCTCCCGGAGCTCGGAGGCGAGAG 1020  
Db 961 GTCAATGAGACCTCCCTCAATGCTGAGTGGAGTGGACCTCCCGGAGCTCGGAGGCGAGAG 1020  
QY 1021 GACCTGTCTACACATCATCTGTGCAAGAGACTGTGCTGGGCGGGGCTCTGCAACCGC 1080  
Db 1021 GACCTGTCTACACATCATCTGTGCAAGAGACTGTGCTGGGCGGGGCTCTGCAACCGC 1080  
QY 1081 TCGGGGAGCAATGTACGTAGCAGCAGCTAGAGGCTTACCGAGGCAATTTAC 1140  
Db 1081 TCGGGGAGCAATGTACGTAGCAGCAGCTAGAGGCTTACCGAGGCAATTTAC 1140  
QY 1141 ATCAGTGAACCTGTGGCCACAGCAGTACACTTCGAAATCCAGGCTGTGAAGGCGTT 1200  
Db 1141 ATCAGTGAACCTGTGGCCACAGCAGTACACTTCGAAATCCAGGCTGTGAAGGCGTT 1200

Db 1141 ATCAGTGAACCTGTGGCCACAGCAGTACACTTCGAAATCCAGGCTGTGAAGGCGTT 1200  
QY 1201 ACTGACCAAGCCCTTCTGCGCTCAAGTTGCTGTGAAATCACCACCAACGAGCA 1260  
Db 1201 ACTGACCAAGCCCTTCTGCGCTCAAGTTGCTGTGAAATCACCACCAACGAGCA 1260  
QY 1261 GCTTCATCGGAGTGTCCATCATGATCAGTGAAGCGGCAACCGTGTGACATTTACCTG 1320  
Db 1261 GCTTCATCGGAGTGTCCATCATGATCAGTGAAGCGGCAACCGTGTGACATTTACCTG 1320  
QY 1321 TCGTGTCCAGGCGGACCAAGATGCGGTATCTGTGACTATGAGCTGACATAT 1380  
Db 1321 TCGTGTCCAGGCGGACCAAGATGCGGTATCTGTGACTATGAGCTGACATAT 1380  
QY 1381 GAGAAAGAGCTCAGTGAATCAAGCCACAGCCATAAAGCCCAACACAGGTACG 1440  
Db 1381 GAGAAAGAGCTCAGTGAATCAAGCCACAGCCATAAAGCCCAACACAGGTACG 1440  
QY 1441 GGCCTCAAGCGGCGGACATATATGCTTCCAGTGTGGGCGAGCACTGTGGAGGCTAC 1500  
Db 1441 GGCCTCAAGCGGCGGACATATATGCTTCCAGTGTGGGCGAGCACTGTGGAGGCTAC 1500  
QY 1501 GGGCGCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAACCGAGAACG 1560  
Db 1501 GGGCGCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAACCGAGAACG 1560  
QY 1561 ATCCAGAGAAATTTGCATCATATGCGCTCTCGGCGGCTGGCTGTCTCTCAT 1620  
Db 1561 ATCCAGAGAAATTTGCATCATATGCGCTCTCGGCGGCTGGCTGTCTCTCAT 1620  
QY 1621 GCTGTGTTGTATGCGCATGCTGTGTAAACAGAGGGGGTTGAGGCTGTGCTGAG 1680  
Db 1621 GCTGTGTTGTATGCGCATGCTGTGTAAACAGAGGGGGTTGAGGCTGTGCTGAG 1680  
QY 1681 TACACGAGAAAGCTTCAACACTACACAGTGGCCACATTAACCCAGCATGAAGATCTAC 1740  
Db 1681 TACACGAGAAAGCTTCAACACTACACAGTGGCCACATTAACCCAGCATGAAGATCTAC 1740  
QY 1741 ATCGATCTTTCACTACAGAGACCCCAAGAGGCACTGCGGAGTTTCCAAAGAAAT 1800  
Db 1741 ATCGATCTTTCACTACAGAGACCCCAAGAGGCACTGCGGAGTTTCCAAAGAAAT 1800  
QY 1801 GACATCTCTGTGTCAAAATTTGAGAGGTGATCGGAGGAGGAGTTTGGGAGGCTGTC 1860  
Db 1801 GACATCTCTGTGTCAAAATTTGAGAGGTGATCGGAGGAGGAGTTTGGGAGGCTGTC 1860  
QY 1861 AGTGGCCACCTGAAGCTGCGAGGCAAGAGAGATCTTGTGGCATCAAGACGCTCAAG 1920  
Db 1861 AGTGGCCACCTGAAGCTGCGAGGCAAGAGAGATCTTGTGGCATCAAGACGCTCAAG 1920  
QY 1921 TCGGGGTACAGGAGAGAGAGGCGGCGGACTTCTGAGGGAAGCCCTCATTCATGGGCCAG 1980  
Db 1921 TCGGGGTACAGGAGAGAGAGGCGGCGGACTTCTGAGGGAAGCCCTCATTCATGGGCCAG 1980  
QY 1981 TTGACCATCCCAACGTATCCACTGAGAGGTGTGCTGACCAAGAGCACACTGTGATG 2040  
Db 1981 TTGACCATCCCAACGTATCCACTGAGAGGTGTGCTGACCAAGAGCACACTGTGATG 2040  
QY 2041 ATCATACCGAGTTATGAGAGATGGCTCTGAGCTCTCTTCTCCGGCAAAACGATGGG 2100  
Db 2041 ATCATACCGAGTTATGAGAGATGGCTCTGAGCTCTCTTCTCCGGCAAAACGATGGG 2100  
QY 2101 CAGTTACAGATCATCAGTGTGTGGGCAATGCTTGGGGGCAATGCGAGCTGGAATGAGTAC 2160  
Db 2101 CAGTTACAGATCATCAGTGTGTGGGCAATGCTTGGGGGCAATGCGAGCTGGAATGAGTAC 2160  
QY 2161 CTGGAGAGATGAATATGTTACCGGTGACCTGTGCGCGCAACATCTGTCTAACAGC 2220  
Db 2161 CTGGAGAGATGAATATGTTACCGGTGACCTGTGCGCGCAACATCTGTCTAACAGC 2220  
QY 2221 AACCTGTCTGAAAGGTGTGAGCTTTGGGCTCTACGCTTTCTAGAGAGAGATACCTCA 2280  
Db 2221 AACCTGTCTGAAAGGTGTGAGCTTTGGGCTCTACGCTTTCTAGAGAGAGATACCTCA 2280

OY 2281 GACCCACCTACACAGTGGCTGGGCGGAAATTCCCATCCGCTGGACAGCCCCGGAA 2340  
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DB 2281 GACCCACCTACACAGTGGCTGGGCGGAAATTCCCATCCGCTGGACAGCCCCGGAA 2340  
OY 2341 GCCATCCAGTACCGGAAATTCACCTCGGCGAGTGTGTGGAGCTACGGCATTTCTCATG 2400  
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DB 2341 GCCATCCAGTACCGGAAATTCACCTCGGCGAGTGTGTGGAGCTACGGCATTTCTCATG 2400  
OY 2401 TGGGAGGTGATGTCTTATGGGAGGCGGCTACGTGGGACATGACCAACAGAGATTAATC 2460  
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DB 2401 TGGGAGGTGATGTCTTATGGGAGGCGGCTACGTGGGACATGACCAACAGAGATTAATC 2460  
OY 2461 AATGCCATTGAGCAGAGATATCGCTGCCACCGCCCATGAGACTGGCCGAGCGCCCTGCAC 2520  
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DB 2461 AATGCCATTGAGCAGAGATATCGCTGCCACCGCCCATGAGACTGGCCGAGCGCCCTGCAC 2520  
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DB 2521 CAATCATGTGCTGAGCTGTTGGCAGAAAGCAGCAACACCGGCCCAAGTTGGCCCAATT 2580  
OY 2581 GTCAACACGCTAGACAAAGATGATCCGCAATCCCAACAGGCTCAAAAGCCATGGCGCCCTC 2640  
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DB 2581 GTCAACACGCTAGACAAAGATGATCCGCAATCCCAACAGGCTCAAAAGCCATGGCGCCCTC 2640  
OY 2641 TCCTGTGCGATCAACCTGCGCTGTGACCGACGATCCCGACTACACAGCTTTAAC 2700  
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DB 2641 TCCTGTGCGATCAACCTGCGCTGTGACCGACGATCCCGACTACACAGCTTTAAC 2700  
OY 2701 ACGGTGACAGTGGCTGGAGCCCATCAAGATGGGCGAGTACAAAGAGAGCTTCCGCAAT 2760  
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DB 2701 ACGGTGACAGTGGCTGGAGCCCATCAAGATGGGCGAGTACAAAGAGAGCTTCCGCAAT 2760  
OY 2761 GCCGGCTTACCTCTTTCAGTGTGTCTCAGATGATGAGAGACATTTCTCCGGGTT 2820  
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DB 2761 GCCGGCTTACCTCTTTCAGTGTGTCTCAGATGATGAGAGACATTTCTCCGGGTT 2820  
OY 2821 GGGGTCTACTTGGCTGGCCACGAGAAAAAATCTGACAGTATCCAGTGTATGGGGCG 2880  
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DB 2821 GGGGTCTACTTGGCTGGCCACGAGAAAAAATCTGACAGTATCCAGTGTATGGGGCG 2880  
OY 2881 CAGATTAACCAATTCAGTGTGTGGAGTGTGACATTCACCTGGCTACCTCTTC 2940  
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DB 2881 CAGATTAACCAATTCAGTGTGTGGAGTGTGACATTCACCTGGCTACCTCTTC 2940  
OY 2941 CTCGAAGCCCGCCCTCTGC 2962  
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DB 2941 CTCGAAGCCCGCCCTCTGC 2962

RESULT 2  
US-08-702-367A-10  
Sequence 10, Application US/08702367A  
Patent No. 5981246  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehaven Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367A

FILED DATE: 435  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2962 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2913  
US-08-702-367A-10

Query Match 100.0%; Score 2962; DB 2; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGTCGCGCGCGTGGAGAAACGCTTAATGAGACTCCACTACAGGAGCTGTGAGCTGGC 60  
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DB 1 CTGTCGCGCGCGTGGAGAAACGCTTAATGAGACTCCACTACAGGAGCTGTGAGCTGGC 60  
OY 61 TGGATGTGATCTCTTCATCAGGTGGAGAGAGTGAAGTGTGCTACGATGAGAACTGAAAC 120  
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DB 61 TGGATGTGATCTCTTCATCAGGTGGAGAGAGTGAAGTGTGCTACGATGAGAACTGAAAC 120  
OY 121 ACGATCCGACGTAACAGAGTGTGCAAGCTGTTAGTCAAGCCAAACAGCTGGCTAGAG 180  
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DB 121 ACGATCCGACGTAACAGAGTGTGCAAGCTGTTAGTCAAGCCAAACAGCTGGCTAGAG 180  
OY 181 ACCAAGTTTATCCGCGCGCTGGGCGCCACCGCATCAAGTGGAGATGAAGTTTTCGGTG 240  
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DB 181 ACCAAGTTTATCCGCGCGCTGGGCGCCACCGCATCAAGTGGAGATGAAGTTTTCGGTG 240  
OY 241 CGTGAACGACGACATCCCGACGCTGCTGCTCTGCAAGAGAACTTCAACTCTAT 300  
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OY 301 TACTATGAGGCTGATCTTGTGACTCGGCGACCAAGACCTTCCCACTGATGAGAAATCCA 360  
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DB 301 TACTATGAGGCTGATCTTGTGACTCGGCGACCAAGACCTTCCCACTGATGAGAAATCCA 360  
OY 361 TGGGTGAAGTGTGATACATTCGACGCCAGAGAGCTTCTCCAGGTGACCTGGGTGAC 420  
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DB 361 TGGGTGAAGTGTGATACATTCGACGCCAGAGAGCTTCTCCAGGTGACCTGGGTGAC 420  
OY 421 CGCGTCATGAAATCAACACGAGGTGCGGAGCTTCCGACCTGTCTCCGACGCGCTTC 480  
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DB 421 CGCGTCATGAAATCAACACGAGGTGCGGAGCTTCCGACCTGTCTCCGACGCGCTTC 480  
OY 481 TACCTGGCTTCAGAGACTATGGGCGCTGCATGCTCATGCGCGTGTCTTCTTAC 540  
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DB 481 TACCTGGCTTCAGAGACTATGGGCGCTGCATGCTCATGCGCGTGTCTTCTTAC 540  
OY 541 CCGAAGTCCCGCATCATCCAGATGCGGCATCTTCCAGAAACCTGTGCGGGGCT 600  
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DB 541 CCGAAGTCCCGCATCATCCAGATGCGGCATCTTCCAGAAACCTGTGCGGGGCT 600  
OY 601 GAGAGCATGCTGTGTGCTGCGCGGCGGAGCTGATGCCAATGCGGAAGGTGAT 660  
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DB 601 GAGAGCATGCTGTGTGCTGCGCGGCGGAGCTGATGCCAATGCGGAAGGTGAT 660  
OY 661 GTACCCATCAAGCTTACTGTAAGGAGGAGGAGTGTGCTGTGCGGCGCTGC 720  
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DB 661 GTACCCATCAAGCTTACTGTAAGGAGGAGGAGTGTGCTGTGCGGCGCTGC 720  
OY 721 ATGTGAAAGCAGGCTTTCAGAGCGGTTGAAATGCAACCGCTGTGCGAGGTTGCTCATCT 780  
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DB 721 ATGTGAAAGCAGGCTTTCAGAGCGGTTGAAATGCAACCGCTGTGCGAGGTTGCTCATCT 780

QY 781 GGGACCTTCAAGGCCAACCAAGGGATGAGGCGCTGTACCCACTGTGCCATCAACAGCCGG 840  
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Db 781 GGGACTTTCAGAGGCCAACCAAGGGATGAGGCGCTGTACCCACTGTGCCATCAACAGCCGG 840  
QY 841 ACCACTTGTGAAGGGGGCCACCACACTGTGTCTGCCCAATGGCTACTACAGAGAGACCTG 900  
| | | | |  
Db 841 ACCACTTGTGAAGGGGGCCACCACACTGTGTCTGCCCAATGGCTACTACAGAGAGACCTG 900  
QY 901 GACCCCGGAGACATGCCCTGTGACAAACCATCTCCCGGCCCGCCAGGCTGTATTTCCAGT 960  
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Db 901 GACCCCGGAGACATGCCCTGTGACAAACCATCTCCCGGCCCGCCAGGCTGTATTTCCAGT 960  
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Db 1021 GACCTCGTCTCAACATCATCTGTGCAAGAGCTGTGGCTGGGGCCGGGTCCCTGCAACCCG 1080  
QY 1081 TGGCGGACATGTACAGTACGACACACGCGAGCTAGGCGCTGACGAGCCGACATTTAC 1140  
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Db 1081 TGGCGGACATGTACAGTACGACACACGCGAGCTAGGCGCTGACGAGCCGACATTTAC 1140  
QY 1141 ATCAGTGAAGCTGTGGCCACACACAGTACACTTTCGAGATCCAGGCTGTGAGAGCGCTT 1200  
| | | | |  
Db 1141 ATCAGTGAAGCTGTGGCCACACACAGTACACTTTCGAGATCCAGGCTGTGAGAGCGCTT 1200  
QY 1201 ACTGACGAGACCCCTTCTGCGCTCACTGTGCGCTCTGTGAAATCACCACACAGGCA 1260  
| | | | |  
Db 1201 ACTGACGAGACCCCTTCTGCGCTCACTGTGCGCTCTGTGAAATCACCACACAGGCA 1260  
QY 1261 GCTTCATCGGCAAGTGTCCATCATGATCAGTGTGAGCGGACACCGTGGACAGATTAACCTG 1320  
| | | | |  
Db 1261 GCTTCATCGGCAAGTGTCCATCATGATCAGTGTGAGCGGACACCGTGGACAGATTAACCTG 1320  
QY 1321 TCGTGTGCCAGCGGACACAGCCCAATGGCGTATCTGTGAACTATGAGCTGACACTAT 1380  
| | | | |  
Db 1321 TCGTGTGCCAGCGGACACAGCCCAATGGCGTATCTGTGAACTATGAGCTGACACTAT 1380  
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Db 1381 GAGAAAGAGCTGAGTGTACAAAGCCGACAGCCATAAAGCCGACACACAGGCTACG 1440  
QY 1441 GGCCTCAAGCCGGCGCCATCTATGTCTTCAGGTGGGGGAGGAGCACTGTGGAGGCTAC 1500  
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Db 1441 GGCCTCAAGCCGGCGCCATCTATGTCTTCAGGTGGGGGAGGAGCACTGTGGAGGCTAC 1500  
QY 1501 GGGGCTACAGCGGCAAGATGATCTTCACACATGACAGAGCCGAGTACAGACAGC 1560  
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Db 1501 GGGGCTACAGCGGCAAGATGATCTTCACACATGACAGAGCCGAGTACAGACAGC 1560  
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Db 1561 ATCCAGGAGAGTGGCAGTATCATGAGGCTGCGGCGCTGGCGGTGCTTCAT 1620  
QY 1621 GCTGTGTTGTATCGGCATGTGTGTACAGAGGGGGTTTGAAGCTGTGACTGGAG 1680  
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Db 1621 GCTGTGTTGTATCGGCATGTGTGTACAGAGGGGGTTTGAAGCTGTGACTGGAG 1680  
QY 1681 TACAGGAGACAGTGCACATCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740  
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Db 1681 TACAGGAGACAGTGCACATCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740  
QY 1741 ATCGATCTCTTCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
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Db 1741 ATCGATCTCTTCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1801 GACATCTCTGTGTCAAAATTTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
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Db 1801 GACATCTCTGTGTCAAAATTTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860

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Db 1861 AGTGGCCACTGGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAAGAGCCTAAG 1920  
QY 1921 TCGGGCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
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Db 1921 TCGGGCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
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Db 1981 TTGACACATCCCAAGTCAATCAGTGCAGGAGTGTGTGACCAAGAGACAGACCTGTGATG 2040  
QY 2041 ATCATCAACAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
| | | | |  
Db 2041 ATCATCAACAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
QY 2101 CAGTTCAAGTCAATCAAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2160  
| | | | |  
Db 2101 CAGTTCAAGTCAATCAAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2160  
QY 2161 CTGGCAGACATGAATATATTTACACCTGTGACCTGTGACCTGTGACCTGTGACCTGT 2220  
| | | | |  
Db 2161 CTGGCAGACATGAATATATTTACACCTGTGACCTGTGACCTGTGACCTGTGACCTGT 2220  
QY 2221 AACCTGTGTCAAGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2280  
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Db 2221 AACCTGTGTCAAGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2280  
QY 2281 GACCCCACTACACAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2340  
| | | | |  
Db 2281 GACCCCACTACACAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2340  
QY 2341 GCCATCAGTACAGGAGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2400  
| | | | |  
Db 2341 GCCATCAGTACAGGAGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTG 2400  
QY 2401 TGGAGGTGATGTCTATGTGGAGAGCGCCCTACTGTGGAGATGACCAAGAGATTAATC 2460  
| | | | |  
Db 2401 TGGAGGTGATGTCTATGTGGAGAGCGCCCTACTGTGGAGATGACCAAGAGATTAATC 2460  
QY 2461 AATGCCATTGAGAGAGATGTGGCTGTGCCAGCGCCATGAGACTGCCAGAGCGCTGAC 2520  
| | | | |  
Db 2461 AATGCCATTGAGAGAGATGTGGCTGTGCCAGCGCCATGAGACTGCCAGAGCGCTGAC 2520  
QY 2521 CAATCATGTGTGATGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
| | | | |  
Db 2521 CAATCATGTGTGATGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
QY 2581 GTCAACAGCTAGACAAAGATGATCCCAATCCCAAGGCTCAAAAGCATGGCGCCCTC 2640  
| | | | |  
Db 2581 GTCAACAGCTAGACAAAGATGATCCCAATCCCAAGGCTCAAAAGCATGGCGCCCTC 2640  
QY 2641 TCCCTGAGATCACTGCGCGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
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Db 2641 TCCCTGAGATCACTGCGCGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
QY 2701 ACAGTGGAGAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
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Db 2701 ACAGTGGAGAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
QY 2761 GCGGCTTACCTCTTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820  
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Db 2761 GCGGCTTACCTCTTTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820  
QY 2821 GGGGCTACTTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
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Db 2821 GGGGCTACTTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
QY 2881 CAGATGAACAGATTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
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Db 2881 CAGATGAACAGATTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
QY 2941 CTCCAAGCCCGCCCTCTGTG 2962

Db 2941 CTCGAGCCCGCCCTCTGCG 2962

RESULT 3  
PCT-US95-04681-10  
Sequence 10, Application PC/TUS9504681  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Amgen Patent Operations/RBM  
STREET: 1840 Dehaven Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2962 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2913  
PCT-US95-04681-10

Query Match 100.0%; Score 2962; DB 5; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTGCTGCGCGCGTGGAGAAAGCTAATGACTCCACTACAGCGACTGCTGGCG 60  
1 CTGCTGCGCGCGTGGAGAAAGCTAATGACTCCACTACAGCGACTGCTGGCG 60  
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61 TGGATGCTGCTCTCTCATCAGAGTGGGAAAGAGTGGTGGTGGTGGTGGTGG 120  
121 AGCATCGGACGTCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180  
121 AGCATCGGACGTCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180  
121 AGCATCGGACGTCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180  
181 ACCAAGTTATCCGGCGCGTGGGCGCCACCGCATCCAGGTGAGATGAACTTTCG 240  
181 ACCAAGTTATCCGGCGCGTGGGCGCCACCGCATCCAGGTGAGATGAACTTTCG 240  
241 CGGACTGCGACGATCCCGACGTCGCTGCTGGAGAGAGCTTCAACCTCTAT 300  
241 CGGACTGCGACGATCCCGACGTCGCTGCTGGAGAGAGCTTCAACCTCTAT 300  
301 TACTATGAGGCTGACTTTGACTGCGCCACCAAGACCTTCCCAACTGATGGAATCCA 360  
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Db 361 TGGGTGAAGGTGATACCATTCGACGCCGACGAGAGCTTCTCCAGGTGGACTGGGTGGC 420  
421 CGGCTCATGAAATCAACACACGAGTGGAGCTTCCGAGCTGTGTCGCCACGCGCTTC 480  
421 CGGCTCATGAAATCAACACACGAGTGGAGCTTCCGAGCTGTGTCGCCACGCGCTTC 480  
481 TACCTGCTCTTCGACGATATGCGGCGCTGATGCTCTCATGCGCGCTGTCTTAC 540  
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841 ACCACTTTGAAGGGGCGCCACCAACTGTGTGCGCGCAATGGCTCTACAGAGAGACTG 900  
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901 GACCCCTGGACATGCTCTGACAGCAACCATCCCTCCGCGCGCGAGTGTATTTCCAGT 960  
901 GACCCCTGGACATGCTCTGACAGCAACCATCCCTCCGCGCGCGAGTGTATTTCCAGT 960  
961 GTCAATGAGACCTCCCTCATGCTGTGAGTGGACCCCTCCGCGCGAGTGTATTTCCAGT 1020  
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1081 TGGGGGACATGTACAGTACGACGACGACGACGACGACGACGACGACGACGACGAC 1140  
1081 TGGGGGACATGTACAGTACGACGACGACGACGACGACGACGACGACGACGACGAC 1140  
1141 ATCAGTGAAGCTCTGCGCGCACACCGAGTACACCTTCGAGATCGAGGCTGTGAACGCGCTT 1200  
1141 ATCAGTGAAGCTCTGCGCGCACACCGAGTACACCTTCGAGATCGAGGCTGTGAACGCGCTT 1200  
1201 ACTGACAGAGCGCTTCTGCGCTTACGCTGTGAGTACATCAACCAACGAGCA 1260  
1201 ACTGACAGAGCGCTTCTGCGCTTACGCTGTGAGTACATCAACCAACGAGCA 1260  
1261 GGTCCATGGGCGAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
1261 GGTCCATGGGCGAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
1321 TCGTGTCCCAAGCGGACGACGCAATGGCGTGTATCTGAGTATGATGATGATGAT 1380  
1321 TCGTGTCCCAAGCGGACGACGCAATGGCGTGTATCTGAGTATGATGATGATGAT 1380  
1381 GAGAGGAGCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1440  
1381 GAGAGGAGCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1440  
1441 GGCCTCAAGAGCGGCGCATCTATGTCTTCCAGGTGCGGCGACGACTGTGCGAGCTAC 1500  
1441 GGCCTCAAGAGCGGCGCATCTATGTCTTCCAGGTGCGGCGACGACTGTGCGAGCTAC 1500

Db 1441 GGCCTCAAGCCGGCCCATCTATGTCTTCCAGTGTGGGCGACGACATGTGGCAGGCTAC 1500  
 QY 1501 GGGCCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAAGCCGACTACAGCAAGC 1560  
 Db 1501 GGGCCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAAAGCCGACTACAGCAAGC 1560  
 QY 1561 ATCCAGGAGAAAGTGGCCATCTATCATGTGGCTCCCTGGCCGCTGCTGCTCTCTCAAT 1620  
 Db 1561 ATCCAGGAGAAAGTGGCCATCTATCATGTGGCTCCCTGGCCGCTGCTGCTCTCTCAAT 1620  
 QY 1621 GCTGTGGTTCATGCGCATGCTGTGTAAACAGAGCGGGGTTTGGAGCTGTACTCGAG 1680  
 Db 1621 GCTGTGGTTCATGCGCATGCTGTGTAAACAGAGCGGGGTTTGGAGCTGTACTCGAG 1680  
 QY 1681 TACACGCAAGCTGCAACACTACACAGTAGGCCACATATACCCAGGATGAGATCTAC 1740  
 Db 1681 TACACGCAAGCTGCAACACTACACAGTAGGCCACATATACCCAGGATGAGATCTAC 1740  
 QY 1741 ATCGATCTTTCACCTACAGAGAGACCCCAAGAGGCAAGTGGCGAGTTGCCAAGAAAT 1800  
 Db 1741 ATCGATCTTTCACCTACAGAGAGACCCCAAGAGGCAAGTGGCGAGTTGCCAAGAAAT 1800  
 QY 1801 GACATCTCTGTGTCAAATTTAGAGAGGTGATCGAGACAGGGGAGTTGGGAGGCTGC 1860  
 Db 1801 GACATCTCTGTGTCAAATTTAGAGAGGTGATCGAGACAGGGGAGTTGGGAGGCTGC 1860  
 QY 1861 AGTGGCCACTGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAACAGCTCAAG 1920  
 Db 1861 AGTGGCCACTGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCCATCAACAGCTCAAG 1920  
 QY 1921 TCGGGCTACAGGAGAGACCCGGGAGCTTCTGAGCCAGGCTCCATCATGTGGGCGAG 1980  
 Db 1921 TCGGGCTACAGGAGAGACCCGGGAGCTTCTGAGCCAGGCTCCATCATGTGGGCGAG 1980  
 QY 1981 TTGACCATCCCAAGCTATCCAGCTGGAGGGTGTCTGACCAAGACACACCTGTGATG 2040  
 Db 1981 TTGACCATCCCAAGCTATCCAGCTGGAGGGTGTCTGACCAAGACACACCTGTGATG 2040  
 QY 2041 ATCTACCAAGCTATGAGAGATGCTCTCCCTGAGCTCTTCTCCGCAAAAGATGGG 2100  
 Db 2041 ATCTACCAAGCTATGAGAGATGCTCTCCCTGAGCTCTTCTCCGCAAAAGATGGG 2100  
 QY 2101 CAGTTACAGTATCCAGCTGGTGGGATGTTGGGGCAATCCGAGTGGCATGATCAATAC 2160  
 Db 2101 CAGTTACAGTATCCAGCTGGTGGGATGTTGGGGCAATCCGAGTGGCATGATCAATAC 2160  
 QY 2161 CTGGCAGACATGAATGTTTACCGGTGACCTGGCTGCCGCAACATCTCTGTCACAGC 2220  
 Db 2161 CTGGCAGACATGAATGTTTACCGGTGACCTGGCTGCCGCAACATCTCTGTCACAGC 2220  
 QY 2221 AACCTGGTTCGCAAGGTGTGGGACTTGGGCTCTCAGCGCTTTTGAAGAGCATACCTCA 2280  
 Db 2221 AACCTGGTTCGCAAGGTGTGGGACTTGGGCTCTCAGCGCTTTTGAAGAGCATACCTCA 2280  
 QY 2281 GACCCCACTACACAGTGTGGGCGGAAAGTTCCCAATCCGCTGGAAGAGCCCGGAA 2340  
 Db 2281 GACCCCACTACACAGTGTGGGCGGAAAGTTCCCAATCCGCTGGAAGAGCCCGGAA 2340  
 QY 2341 GCCATCCAGTACCGGAATTCACCTGGCCAGTATGTGTGAGCTACGCGCATTTGTATG 2400  
 Db 2341 GCCATCCAGTACCGGAATTCACCTGGCCAGTATGTGTGAGCTACGCGCATTTGTATG 2400  
 QY 2401 TGGGAGGTGATGCTATGGGGAGCGGCTTACTGGGACATGACCAACAGATGTAAATC 2460  
 Db 2401 TGGGAGGTGATGCTATGGGGAGCGGCTTACTGGGACATGACCAACAGATGTAAATC 2460  
 QY 2461 AATGCCATTGAGCAGACTATCGGCTGCCACCGCCATGAGTGGCGGAGCGGCTGCAC 2520  
 Db 2461 AATGCCATTGAGCAGACTATCGGCTGCCACCGCCATGAGTGGCGGAGCGGCTGCAC 2520  
 QY 2521 CAATCATGCTGAGCTGTGGGAGGAAGACCGCAACACCGGCGCAAGTTGGGCCAAAT 2580  
 Db 2521 CAATCATGCTGAGCTGTGGGAGGAAGACCGCAACACCGGCGCAAGTTGGGCCAAAT 2580

QY 2581 GTCAACAGCTAGACAAAGATATCCGCAATCCCAACAGCTCAAAAGCCATGGGCCCCCTC 2640  
 Db 2581 GTCAACAGCTAGACAAAGATATCCGCAATCCCAACAGCTCAAAAGCCATGGGCCCCCTC 2640  
 QY 2641 TCCCTGTGATCAACCTGCGCTCTGTGAGCGGACAGATCCCGGCTCTACACAGCTTAAAC 2700  
 Db 2641 TCCCTGTGATCAACCTGCGCTCTGTGAGCGGACAGATCCCGGCTCTACACAGCTTAAAC 2700  
 QY 2701 ACGTGAAGAGTGGCTGAGAGGCCATCAAGATGGGGGACAGTACAGAGAGCTTGGCCAA 2760  
 Db 2701 ACGTGAAGAGTGGCTGAGAGGCCATCAAGATGGGGGACAGTACAGAGAGCTTGGCCAA 2760  
 QY 2761 GCGGGCTTCACTCTCTTGTGAGCTGTCTGTCAAGTATGATGAGAGGACATTTCCGGGTT 2820  
 Db 2761 GCGGGCTTCACTCTCTTGTGAGCTGTCTGTCAAGTATGATGAGAGGACATTTCCGGGTT 2820  
 QY 2821 GGGGTCACTTTGGCTGGCCACAGAAAAAATCCTGAACAGTATCCAGTGTATGGGGGCG 2880  
 Db 2821 GGGGTCACTTTGGCTGGCCACAGAAAAAATCCTGAACAGTATCCAGTGTATGGGGGCG 2880  
 QY 2881 CAGATGAACCAAGATTCAGTGTGAGAGTTTGAACATTCACCTGCTGGCTCACTCTTC 2940  
 Db 2881 CAGATGAACCAAGATTCAGTGTGAGAGTTTGAACATTCACCTGCTGGCTCACTCTTC 2940  
 QY 2941 CTCCAAGCCCCGCCCTCTGC 2962  
 Db 2941 CTCCAAGCCCCGCCCTCTGC 2962

RESULT 4  
 US-08-542-635-1  
 ; Sequence 1, Application US/08542635  
 ; Patent No. 6218356  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pawson, Anthony  
 ; APPLICANT: Henkemeier, Mark  
 ; APPLICANT: Letwin, Kenneth  
 ; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bereskin & Parr  
 ; STREET: 40 King Street West, Box 401  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: M5H 3Y2  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/542,635  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McDiarmid, Shona S.  
 ; REGISTRATION NUMBER: 38,798  
 ; REFERENCE/DOCKET NUMBER: 3153-162  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (416) 364-7311  
 ; TELEFAX: (416) 361-1398  
 ; TELEX: 06-23115  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3105 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:



ORGANISM: Mus musculus  
DEVELOPMENTAL STAGE: Embryo  
IMMEDIATE SOURCE:  
LIBRARY: lambda gt10 cDNA library  
CLONE: combined PHUKACE A2 and K2 AND cDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Distal end of chromosome 4  
MAP POSITION: near the abd-1 mutation  
US-08-542-635-1

Query Match 1.6%; Score 48; DB 4; Length 3105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1440 GGGCCCAAGCCGGCCATCATCTCTCCAGTGGGGGCGAC 1487  
|||||  
Db 1512 GGGCCCAAGCCGGCCATCATCTCTCCAGTGGGGGCGAC 1559

## RESULT 5

US-08-469-537A-28  
Sequence 28, Application US/08469537A  
Patent No. 5843749  
GENERAL INFORMATION:  
APPLICANT: Maisongier, et al.  
TITLE OF INVENTION: EHK AND ROR TYROSINE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/406,247  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: USN 08/144,992  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USN 07/736,559  
FILING DATE: 26-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempier, Ph.D., Gall M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 070C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
TELEX:  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..162  
US-08-469-537A-28

Query Match 1.2%; Score 35; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2206 ATCTGTCAACAGCACTGTCTGCAAGTGTG 2240  
|||||  
Db 1 ATCTGTCAACAGCACTGTCTGCAAGTGTG 35

## RESULT 6

US-08-162-809-7  
Sequence 7, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereydoon G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3776 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 290..3208  
US-08-162-809-7

Query Match 1.1%; Score 32; DB 1; Length 3776;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2389 GGCATTGTCTGGAGAGTGATGCTATG 2420  
|||||  
Db 2687 GGCATTGTCTGGAGAGTGATGCTATG 2718

## RESULT 7

US-08-162-809-1  
Sequence 1, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereydoon G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CAMPBELL AND FLORES  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 92122  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentln Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/162,809  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 9503  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3133 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: join(3..419, 421..2858)  
;;  
US-08-162-809-1

Query Match 1.0%; Score 29; DB 1; Length 3133;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GGCTCTGCGAGAGACCTTCACCTCTA 299  
|||||  
DB 255 GGCTCTGCGAGAGACCTTCACCTCTA 283

RESULT 8  
US-08-469-537A-100  
; Sequence 100, Application US/08469537A  
; Patent No. 5843749  
; GENERAL INFORMATION:  
; APPLICANT: Maisongierre, et al.  
; TITLE OF INVENTION: EHK AND ROR TYROSINE  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,537A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/406,247  
; FILING DATE: 17-MAR-1995  
; APPLICATION NUMBER: USSN 08/144,992

;; FILING DATE: 28-OCT-1993  
;; APPLICATION NUMBER: USSN 07/736,559  
;; FILING DATE: 26-JUL-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Kempler, Ph.D., Gail M  
;; REGISTRATION NUMBER: 32,143  
;; REFERENCE/DOCKET NUMBER: REG 070C  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 914-345-7400  
;; TELEFAX: 914-345-7721  
;;  
;; INFORMATION FOR SEQ ID NO: 100:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3592 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; MOLECULE TYPE: DNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 598..3444  
;;  
;; FEATURE:  
;; NAME/KEY: modified\_base  
;; LOCATION: 56  
;; OTHER INFORMATION: /mod\_base= OTHER  
;; OTHER INFORMATION: /label= N  
;; OTHER INFORMATION: /note= "Where N = G, A, C or T"  
;;  
;; FEATURE:  
;; NAME/KEY: modified\_base  
;; LOCATION: 3538  
;; OTHER INFORMATION: /mod\_base= OTHER  
;; OTHER INFORMATION: /label= N  
;; OTHER INFORMATION: /note= "Where N = G, A, C or T"  
;;  
US-08-469-537A-100

Query Match 1.0%; Score 29; DB 2; Length 3592;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2392 ATTGTCATGTGGAGAGTGATGCTATGG 2420  
|||||  
DB 3184 ATTGTCATGTGGAGAGTGATGCTATGG 3212

RESULT 9  
US-08-162-809-17  
; Sequence 17, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pasquale, Elena B.  
; TITLE OF INVENTION: NOVEL BPH-RELATED TYROSINE KINASES,  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,809  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4049 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..2994  
US-08-162-809-17

Query Match 1.0%; Score 29; DB 1; Length 4049;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2212 GTCACAGCAACCTGCTGCAAGGTGC 2240  
DB 2296 GTCACAGCAACCTGCTGCAAGGTGC 2324

RESULT 10  
US-08-162-809-11  
Sequence 11, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjad, Fereydon G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4097 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 10..3042  
US-08-162-809-11

Query Match 1.0%; Score 29; DB 1; Length 4097;  
Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2212 GTCACAGCAACCTGCTGCAAGGTGC 2240  
DB 2344 GTCACAGCAACCTGCTGCAAGGTGC 2372

RESULT 11  
US-08-449-645A-23/c  
Sequence 23, Application US/08449645A  
Patent No. 5981245  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-449-645A-23

Query Match 0.8%; Score 25; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1549 TACACAGACATCCAGGAGACT 1573  
DB 39 TACACAGACATCCAGGAGACT 15

RESULT 12  
US-08-702-367A-23/c  
Sequence 23, Application US/08702367A  
Patent No. 5981246  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-702-367A-23

Query Match 0.8%; Score 25; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 TACCAGACAAGCATCCAGAGAACT 1573  
|||||

DB 39 TACCAGACAAGCATCCAGAGAACT 15

RESULT 13  
PCT-US95-04681-23/c  
Sequence 23, Application PC/TUS9504681  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-04681-23

Query Match 0.8%; Score 25; DB 5; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 TACCAGACAAGCATCCAGAGAACT 1573  
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DB 39 TACCAGACAAGCATCCAGAGAACT 15

RESULT 14  
US-08-469-537A-65  
Sequence 65, Application US/08469537A  
Patent No. 5843749  
GENERAL INFORMATION:  
APPLICANT: Maisonnier, et al.  
TITLE OF INVENTION: EHK AND FOR TYROSINE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/406,247  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: USSN 08/144,992  
FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USSN 07/736,559  
FILING DATE: 26-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Kempler, Ph.D., Gall M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 070C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
TELEX:  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..81  
US-08-469-537A-65

Query Match 0.8%; Score 25; DB 2; Length 81;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2180 TTCACCGTGACCTGGCTGCCGCCAA 2204  
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DB 11 TTCACCGTGACCTGGCTGCCGCCAA 35

RESULT 15  
US-08-162-809-9  
Sequence 9, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Fereyoun G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CAMPBELL AND FLORES  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/162,809  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 9503  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 3546 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 2..2920  
;; US-08-162-809-9

Query Match 0.88; Score 25; DB 1; Length 3546;  
Best Local Similarity 100.0%; Pred. No. 0 012;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1163 CCCAGTACACCTTCGAGATCCAGGC 1187  
|||  
Db 1176 CCCAGTACACCTTCGAGATCCAGGC 1200

Search completed: July 10, 2001, 21:18:55  
Job time: 9477 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 18:34:08 ; Search time 2159.53 Seconds  
(without alignments)  
12965.484 Million cell updates/sec

Title: US-09-378-759-10  
Perfect score: 2962  
Sequence: 1 CTGCTCGCCGCCGTCGAGA.....CCAAAGCCCCGCCCTCTGC 2962

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 0

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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7: gb\_est7:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





QY 2380 TGGAGCTAC 2388  
 Db 681 TGGAGCTAC 689

RESULT 2  
 BE314746 769 bp mRNA EST 26-OCT-2000  
 LOCUS 60114809F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3501578 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BE314746  
 VERSION BE314746.1 GI:9136248  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 769)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: L1CM172 row: a column: 03  
 High quality sequence start: 16  
 High quality sequence stop: 683.  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3501578"  
 /clone\_1lb="NIH\_MGC\_19"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: brain; Vector: pOTB7; Site:1: XhoI; Site:2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 162 a 254 c 214 g 139 t

Query Match 14.8%; Score 437; DB 166; Length 769;  
 Best Local Similarity 99.8%; Pred. No. 3.7e-227;  
 Matches 557; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 697 TGGCTGTGCGCATTCGGGGCGCTGCATGTGAAGCAGGCTTCAGAGCCGTGTGGAATGGC 756  
 Db 61 TGGCTGTGCGCATTCGGGGCGCTGCATGTGAAGCAGGCTTCAGAGCCGTGTGGAATGGC 120

QY 757 ACCGCTTGCGAGGTGTCCATCTGGGACTTCAAGGCCAACCAAGGGATGAGGCTGTG 816  
 Db 121 ACCGCTTGCGAGGTGTCCATCTGGGACTTCAAGGCCAACCAAGGGATGAGGCTGTG 180

QY 817 ACCCATGTGCCATCAACAGCCGAGCCACTTCTGAAGGGGACCAACTGTGTCTGCCG 876  
 Db 181 ACCCATGTGCCATCAACAGCCGAGCCACTTCTGAAGGGGACCAACTGTGTCTGCCG 240

QY 877 AATGGCTACTACAGACACACCTGGAGCCCGCTGGACATGCCCTGCACACATCCCTTC 936  
 Db 241 AATGGCTACTACAGACACACCTGGAGCCCGCTGGACATGCCCTGCACACATCCCTTC 300

QY 937 GGGCCCCAGGCTGTGATTTCCAGTGTCAATGAGACCTCCCTCATGTGTGAGTGGACCCCT 996

Db 301 GGGCCCCAGGCTGTGATTTCCAGTGTCAATGAGACCTCCCTCATGTGTGAGTGGACCCCT 360  
 QY 997 CCGCGAGACTCCGGA-GGCGAGAGAGACCTGCTTACAACTATCTGCAAGAGCTGTGG 1055  
 Db 361 CCGCGAGACTCCGGAATGGCCGAGAGACCTGCTTACAACTATCTGCAAGAGCTGTGG 420  
 QY 1056 CTCGGGCGGGGCTCTGTCACACCCGCTGGGGAGACATGTACAGTACACACCCAGCT 1115  
 Db 421 CTCGGGCGGGGCTCTGTCACACCCGCTGGGGAGACATGTACAGTACACACCCAGCT 480

QY 1116 AGGCTGACGAGC CAGGATTTTACATCATGAGTACCTGTGGCCACACCCAGTACACTT 1175  
 Db 481 AGGCTGACGAGC CAGGATTTTACATCATGAGTACCTGTGGCCACACCCAGTACACTT 540

QY 1176 CGAGATCCAGGCTGTGAAGCGGCTTACTGACACAGAGCCCTTCTGCGCTCAGTTGGCTC 1235  
 Db 541 CGAGATCCAGGCTGTGAAGCGGCTTACTGACACAGAGCCCTTCTGCGCTCAGTTGGCTC 600

QY 1236 TGTGAACATCACCAACCA 1253  
 Db 601 TGTGAACATCACCAACCA 618

RESULT 3  
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 LOCUS BG425170 916 bp mRNA EST 14-MAR-2001  
 DEFINITION 60244663F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4585526 5',  
 mRNA sequence.  
 ACCESSION BG425170  
 VERSION BG425170.1 GI:13331676  
 KEYWORDS EST.  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 916)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: L1CM1312 row: m column: 15  
 High quality sequence stop: 726.  
 Location/Qualifiers  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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 /clone\_1lb="NIH\_MGC\_14"  
 /tissue\_type="renal cell adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: kidney; Vector: pOTB7; Site:1: XhoI; Site:2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
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 /organism="Homo sapiens"  
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 /note="Organ: kidney; Vector: pOTB7; Site:1: XhoI; Site:2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 221 a 251 c 284 g 160 t

Query Match 13.7%; Score 406; DB 153; Length 916;  
 Best Local Similarity 99.7%; Pred. No. 3.4e-210;

Matches 576; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1489 GTGGAGGCTACGGGCGCTACAGCGGCAAGTGTACTTCCAGACCTGACGAGAGCCGAG 1548

DB 7 GTGGAGGCTACGGGCGCTACAGCGGCAAGTGTACTTCCAGACCTGACGAGAGCCGAG 66

OY 1549 TACGACACACATCCAGAGAGAGTGGCACTCATCATCGGCTCTCGGCGCTGCGCTG 1608

DB 67 TACGACACACATCCAGAGAGAGTGGCACTCATCATCGGCTCTCGGCGCTGCGCTG 126

OY 1609 GTCTTCTCATTTGCTGTGTGTATCGCATCGTGTGTATACAGAGCGGCTTTGAGCCT 1668

DB 127 GTCTTCTCATTTGCTGTGTGTATCGCATCGTGTGTATACAGAGCGGCTTTGAGCCT 186

OY 1669 GCTGCTGAGATACAGGCAAGCTGCAACATACACATGAGGCAATACCCAGAGC 1728

DB 187 GCTGCTGAGATACAGGCAAGCTGCAACATACACATGAGGCAATACCCAGAGC 246

OY 1729 ATGAAGATCTACATGATCTCTTCACTACAGAGAGCCCAAGAGAGAGTGGAGTTT 1788

DB 247 ATGAAGATCTACATGATCTCTTCACTACAGAGAGCCCAAGAGAGAGTGGAGTTT 306

OY 1789 GCCAAGAAATTCATCTCTCTGTCTCAAAATTCAGAGAGTGTATGAGAGAGAGTTT 1848

DB 307 GCCAAGAAATTCATCTCTCTGTCTCAAAATTCAGAGAGTGTATGAGAGAGAGTTT 365

OY 1849 GCGGAGGCTGCTGAGTGGGACCTGAAAGTGGCAGAGAGAGAGATCTTTTGGCATT 1908

DB 366 GCGGAGGCTGCTGAGTGGGACCTGAAAGTGGCAGAGAGAGAGATCTTTTGGCATT 425

OY 1909 AAGAGCTCAAGTGGGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1968

DB 426 AAGAGCTCAAGTGGGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485

OY 1969 ATCATGAGGCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2028

DB 486 ATCATGAGGCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545

OY 2029 ACACGTGTATGATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2066

DB 546 ACACGTGTATGATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583

RESULT 4 BE256685 523 bp mRNA EST 13-JUL-2000

LOCUS 60110774E1 NIH\_MGC\_16 Homo sapiens cDNA clone IMAGE:343843 5'

DEFINITION mRNA sequence.

ACCESSION BE256685

VERSION BE256685.1 GI:9127149

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.

JOURNAL 1 (bases 1 to 523)

COMMENT Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cga@bbs-riemail.nih.gov

TISSUE Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov

plate: L1CM129 row: d column: 20

High quality sequence stop: 522.

Location/Qualifiers

1..523

/clone="IMAGE:343843"

/clone\_lib="NIH\_MGC\_16"

/lssue\_type="retinoblastoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pORF1; Site\_1: XhoI; Site\_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGGCAGG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH-MGC library."

BASE COUNT 107 a 189 c 135 g 92 t

ORIGIN

Query Match 13.0%; Score 384; DB 165; Length 523;

Best Local Similarity 100.0%; Pred. No. 3.5e-198;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 971 CCTCCCTCATGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1030

DB 140 CCTCCCTCATGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 199

OY 1031 ACAACATCATCTGCAAGAGCTGTGTGCTGCGGCGGCGGCTGTGTGACCCCTGCGGGGACA 1090

DB 200 ACAACATCATCTGCAAGAGCTGTGTGCTGCGGCGGCGGCTGTGTGACCCGCTGCGGGGACA 259

OY 1091 ATGACAGTATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1150

DB 260 ATGACAGTATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 319

OY 1151 TGTGCGCCACACACACACACACACACACACACACACACACACACACACACACACACACAC 1210

DB 320 TGTGCGCCACACACACACACACACACACACACACACACACACACACACACACACACACAC 379

OY 1211 GCCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1270

DB 380 GCCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439

OY 1271 CAGTGTCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1330

DB 440 CAGTGTCCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499

OY 1331 AGCCGACACACACACACACACACACACACACACACACACACACACACACACACACAC 1354

DB 500 AGCCGACACACACACACACACACACACACACACACACACACACACACACACACACAC 523

RESULT 5 AM806532 588 bp mRNA EST 17-MAY-2000

LOCUS I10-ST0002-160599-012 ST0002 Homo sapiens cDNA, mRNA sequence.

DEFINITION AM806532

ACCESSION AM806532

VERSION AM806532.1 GI:7899531

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 588)

Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brustein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?lt=6t2-IL0-ST0002-160-  
599-012&t3=1999-05-16&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 589.

## FEATURES

Source

1. 588

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="ST0002"

/dev\_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site\_1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

Location/Qualifiers

BASE COUNT 111 a 152 c 192 g 133 t

ORIGIN

## Query Match

Best Local Similarity 12.4%; Score 366; DB 120; Length 588;

Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2141 TCGCAGCTGGCATGACATGACCTGGCAGACATGAACTATGTTACACCTGGCTGCTCCC 2200  
|||||  
519 TCGCAGCTGGCATGACATGACCTGGCAGACATGAACTATGTTACACCTGGCTGCTCCC 460  
|||||  
2201 GCACATCTCTGTCACACAGCAACCTGCTGTCGCAAGTGTGCGACTTGGCTCTCAGCCT 2260  
|||||  
459 GCACATCTCTGTCACACAGCAACCTGCTGTCGCAAGTGTGCGACTTGGCTCTCAGCCT 400  
|||||  
2261 TTCTAGAGAGCATGACCTGACACCCACCTACACACCTGGCTGGGGGAAAGTCCCA 2220  
|||||  
399 TTCTAGAGAGCATGACCTGACACCCACCTACACACCTGGCTGGGGGAAAGTCCCA 340  
|||||  
2321 TCGCCTGGACAGCCCGGAAAGCCATCCATGACCGGAAGTTACCTGGCCAGTGTGT 2380  
|||||  
339 TCGCCTGGACAGCCCGGAAAGCCATCCATGACCGGAAGTTACCTGGCCAGTGTGT 280  
|||||  
2381 GGAGCTACGGCATTTGTCATGTTGGAGGTGATGTCCTATGAGGAGCGCCCTACTGGACA 2440  
|||||  
279 GGAGCTACGGCATTTGTCATGTTGGAGGTGATGTCCTATGAGGAGCGCCCTACTGGACA 220  
|||||  
2441 TGACCAACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2500  
|||||  
219 TGACCAACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 160  
|||||  
2501 ACTGCGGAGCGCCCTGACACCACTGCTGAGCTGTTGGCAGAAAGACCGCCACACCC 2560  
|||||  
159 ACCGCGGAGCGCCCTGACACCACTGCTGAGCTGTTGGCAGAAAGACCGCCACACCC 100  
|||||  
2561 GGCGCAAGTTCGGCCCAATTTGTCACACCGCTAGACAAAGATGATGCCAATCCCAACAGCC 2620  
|||||  
99 GGCGCAAGTTCGGCCCAATTTGTCACACCGCTAGACAAAGATGATGCCAATCCCAACAGCC 40  
|||||  
2621 TCAAAAGCATGGGCGCCCTCTCTCTGCGATCAACCTGC 2659  
|||||  
39 TCAAAAGCATGGGCGCCCTCTCTCTGCGATCAACCTGC 1

RESULT 6  
AL040428/c 800 bp mRNA EST 29-FEB-2000  
LOCUS AL040428 800 bp mRNA EST 29-FEB-2000

## DEFINITION

DKFZp434C1814.s1.434 (synonym: htes3) Homo sapiens cDNA clone

## ACCESSION

DKFZp434C1814.3', mRNA sequence.

## VERSION

AL040428.1 GI:5409379

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

Am Kioferspitz 18a D-82152 Martinsried, Germany

## AUTHORS

Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

## TITLE

EST (Koehler, et al.)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Koehler K

## FEATURES

Source

1. 800

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="DKFZp434C1814"

/clone.lib="434 (synonym: htes3)"

/tissue.type="testis"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Vector: pSPori1; Site\_1: NotI; Site\_2: SalI"

## BASE COUNT

193 a 223 c 198 g 186 t

ORIGIN

## Query Match

Best Local Similarity 11.1%; Score 328; DB 105; Length 800;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

444 GGTGCGAGCTTGCGACCTGTGTCGCGCAGCGGCTTCACTGGCCCTTCAGAGCATG 503  
|||||  
768 GTGCGGAGCTTGCGACCTGTGTCGCGCAGCGGCTTCACTGGCCCTTCAGAGCATG 709  
|||||  
504 CGGCTCATGTCCTTCATGCGCGTGGCTGTTCTACCGCAAGTGGCCCGCATATCCA 563  
|||||  
708 CGGCTCATGTCCTTCATGCGCGTGGCTGTTCTACCGCAAGTGGCCCGCATATCCA 649  
|||||  
564 GAATGGCGCATCTTCCAGAAACCTGTGCGGGGTGAGACACATGCTGTGGCTGC 623  
|||||  
648 GAATGGCGCATCTTCCAGAAACCTGTGCGGGGTGAGACACATGCTGTGGCTGC 589  
|||||  
624 CCGGGCAGCTCATGCGCAATGCGGAAGAGTGTGATGATGATGATGATGATGATGATGATG 683  
|||||  
588 CCGGGCAGCTCATGCGCAATGCGGAAGAGTGTGATGATGATGATGATGATGATGATGATG 529  
|||||  
684 CGGGGAGCGGAGTGTGCTGTCGCCATCGGGGCTGTCATGTGTCAAAGAGCTTGAGGC 743  
|||||  
528 CGGGGAGCGGAGTGTGCTGTCGCCATCGGGGCTGTCATGTGTCAAAGAGCTTGAGGC 469  
|||||  
744 CGTTGAGATGGCACGCTGCGGAGGT 771  
|||||  
468 CGTTGAGATGGCACGCTGCGGAGGT 441

RESULT 7  
A1940301/c 325 bp mRNA EST 03-AUG-1999  
LOCUS A1940301 325 bp mRNA EST 03-AUG-1999  
DEFINITION CM2-CT0040-230799-001-A02 CT0040 Homo sapiens cDNA, mRNA sequence.

ACCESSION AT1940301  
VERSION AT1940301.1 GI:5687282  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 325)  
AUTHORS HCCP <http://www.ludwig.org.br/ORESTES>.  
TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-CT0040-230799-001-A02&f3=1999-07-23&tl4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 325.  
Location/Qualifiers  
1..325  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0040"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 58 a 85 c 104 g 78 t  
ORIGIN  
Query Match 10.9%; Score 323; DB 104; Length 325;  
Best Local Similarity 100.0%; Pred. No. 7.9e-165;  
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2335 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGCATGATGTGGAGTACGGCATT 2394  
DB 325 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGCATGATGTGGAGTACGGCATT 266  
OY 2395 GTCATGTGGAGGTATGTCTATGGGAGCGGCCCTACTGGAGATGACCAACGAGAT 2454  
DB 265 GTCATGTGGAGGTATGTCTATGGGAGCGGCCCTACTGGAGATGACCAACGAGAT 206  
OY 2455 GTATTCATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCGAGCGCC 2514  
DB 205 GTAAATCAATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCGAGCGCC 146  
OY 2515 CTGCACCACTCATCTGTGAGACTGTTGGCAGAAAGACCGCAACACCGGCGCCCAAGTTCCGC 2574  
DB 145 CTGCACCACTCATCTGTGAGACTGTTGGCAGAAAGACCGCAACACCGGCGCCCAAGTTCCGC 86  
OY 2575 CAATTTGTCACACGCTAGACAAAGATGATCCGCAATCCCAACAGCCCTCAAAAGCCATGGCG 2634  
DB 85 CAATTTGTCACACGCTAGACAAAGATGATCCGCAATCCCAACAGCCCTCAAAAGCCATGGCG 26  
OY 2635 CCCCTCTCTCTGTGGCATCAACT 2657  
DB 25 CCCCTCTCTCTGTGGCATCAACT 3

LOCUS AM845008 448 bp mRNA EST 19-MAY-2000  
DEFINITION RC0-CP0002-310599-003 CT0002 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM845008  
VERSION AM845008.1 GI:7940434  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 448)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zaio,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
2020263  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0-CT0002-310599-003&f3=1999-05-31&tl4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 12  
High quality sequence stop: 387.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CP0002"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 81 a 116 c 143 g 106 t 2 others  
ORIGIN  
Query Match 10.9%; Score 323; DB 121; Length 448;  
Best Local Similarity 100.0%; Pred. No. 8.1e-165;  
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2335 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGCATGATGTGGAGTACGGCATT 2394  
DB 325 CCGGAAGCCATCCAGTACCGGAAGTTCACTCGGCGCATGATGTGGAGTACGGCATT 266  
OY 2395 GTCATGTGGAGGTATGTCTATGGGAGCGGCCCTACTGGAGATGACCAACGAGAT 2454  
DB 265 GTCATGTGGAGGTATGTCTATGGGAGCGGCCCTACTGGAGATGACCAACGAGAT 206  
OY 2455 GTAAATCAATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCGAGCGCC 2514  
DB 205 GTAAATCAATGCCATTGACAGAGACATATGGCTGCCACCGCCCATGAGTGCCTCGAGCGCC 146  
OY 2515 CTGCACCACTCATCTGTGAGACTGTTGGCAGAAAGACCGCAACACCGGCGCCCAAGTTCCGC 2574  
DB 145 CTGCACCACTCATCTGTGAGACTGTTGGCAGAAAGACCGCAACACCGGCGCCCAAGTTCCGC 86  
OY 2575 CAATTTGTCACACGCTAGACAAAGATGATCCGCAATCCCAACAGCCCTCAAAAGCCATGGCG 2634

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Db 85 CAAATGTCAACAGCTAGACAAAGATGATCCGACATCCCAACAGCTCAAGCATGGCG 26
2635 CCGCTCTCTCTGGCAGCAACCT 2657
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Db 25 CCGCTCTCTCTGGCAGCAACCT 3
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RESULT 9
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LOCUS AM938783
DEFINITION PM3-DT0064-260300-002-f08 DT0064 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM938783
VERSION AM938783.1 GI:8114229
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 517)
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
COMMENT 20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=612-PM3-DT0064-260
300-002-f08&l=3-2000-03-26&l=1)
Seq primer: puc 18 forward
High quality sequence stop: 514.
Location/Qualifiers
1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DT0064"
/dev_stage="Adult"
/notes="Organ: denis.drash; Vector: puc18; Site_1: Smal;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 97 a 133 c 168 g 119 t
ORIGIN

Query Match 10.4%; Score 307; DB 122; Length 517;
Best Local Similarity 99.2%; Pred. No. 4,6e-156;
Matches 507; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2141 TCGCAGCTGGCATGAGTACTGGCAGACATGATGTTACCGTGGCTGGCC 2200
|||||
Db 517 TCGCAGCTGGCATGAGTACTGGCAGACATGATGTTACCGTGGCTGGCC 458
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QY 2201 GCAACATCTCTGTCACAGCAACCTGCTGCAAGGTGTGGACTTTGGCTCTACGCT 2260
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Db 457 GCAACATCTCTGTCACAGCAACCTGCTGCAAGGTGTGGACTTTGGCTCTACGCT 398
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QY 2261 TTCTAGAGAGATNACTCTACAGCCACCTACACCACTGCTGGGGGAAGTTCCCA 2320
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Db 397 TTCTAGAGAGATNACTCTACAGCCACCTACACCACTGCTGGGGGAAGTTCCCA 338
|||||
QY 2321 TCGGCTGACAGCCCGGAAAGCCATCCAGTACGAGGAAGTTACCTGGCGAGTGTGT 2380
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Db 337 TCGGCTGACAGCCCGGAAAGCCATCCAGTACGAGGAAGTTACCTGGCGAGTGTGT 278
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QY 2381 GGAGCTACGCATTTGTCATGTTGGAGGTGATGTCCTTGGGGAGGGCCCTACTGGACA 2440
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Db 277 GGAGCTACGCATTTGTCATGTTGGAGGTGATGTCCTTGGGGAGGGCCCTACTGGACA 218
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QY 2441 TGACCAACAGAGATGTATATCATGATGATGAGCAGATATGCGGTGCCACCGCCATGG 2500
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Db 217 TGACCAACAGAGATGTATATCATGATGATGAGCAGATATGCGGTGCCACCGCCATGG 158
|||||
QY 2501 ACTGCGGAGCGCCCTGACCAACTCATGCTGTGAGCTTTGGCAGAGAGCCGACACCC 2560
|||||
Db 157 ACTGCGGAGCGCCCTGACCAACTCATGCTGTGAGCTTTGGCAGAGAGCCGACACCC 98
|||||
QY 2561 GGGCCAGTTGCGGCAATGTCACACGCTAGACAGATGATCCGATCCCAACAGCC 2620
|||||
Db 97 GGGCCAGTTGCGGCAATGTCACACGCTAGACAGATGATCCGATCCCAACAGCC 38
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QY 2621 TCAAGCCATGCGGCGCCCTCTCTCTGTCGAT 2651
|||||
Db 37 TCAAGCCATGCGGCGCCCTCTCTCTGTCGAT 7
|||||

RESULT 10
BF306234 939 bp mRNA EST 21-NOV-2000
LOCUS BF306234
DEFINITION 601893088F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138988 5',
mRNA sequence.
ACCESSION BF306234
VERSION BF306234.1 GI:11253319
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@dsr-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: LILCM1048 row: o column: 21
High quality sequence stop: 646.
Location/Qualifiers
1..939
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4138988"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(5). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 214 a 261 c 297 g 166 t
ORIGIN

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	/db_xref="taxon:9606"
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	'tissue_type'='colon tumor, RER+'
	/lab_host="DH10B"
	/note="Organ: colon; Vector: p7T7D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI CGAP CO10 was prepared, and ss circles were made in vitro. Following HAM hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneds 1057416-1061255, and 1144584-114531).
	Subtraction by Bento Soares and M. Fatima Bonaldo.
"	
BASE COUNT	104 a      141 c      148 g      103 t
ORIGIN	
Query Match	9.9% Score 292; DB 19; Length 496;
Best Local Similarity:	99.7%; Pred. No. 7,4e-148;
Matches 342;	Conservative : 0; Mismatches 1; Indels 0; Gaps 0;
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OY	210 CCGCATCACAAGTGAGATGAATTTTCGGTGCTGACTGCAGACATCCCCACCGTCCC 269       Db       61 CCGCATCAGAAGTAGATGAATTTTCGGTGCTGACTGCAGACATCCCCACCGTCCC 120
OY	270 TGGCTCTCTGAAGAGAACCTTCAACCTCATATACATATAGGCTCATCTTTCACCTGGCCAC 329     Db       121 TGCTCTCTGAAGAGAACCTTCAACCTCATATATAGGCTCATCTTTCACCTGGCCAC 180
OY	330 CAAGACCTTCCCACTGGATGAGAAATCCATGSGTGTAAGGTGATAACCATTCAGCCGA 369       Db       181 CAAGACCTTCCCACTGGATGAGAAATCCATGSGTGTAAGGTGATAACCATTCAGCCGA 240
OY	390 CGAGAGCTTTCACAGSTGACCTGGGTGGCCGCTCATGAAAATCAAACCGAGGTGGC 449       Db       241 CGAGAGCTTTCACAGSTGACCTGGGTGGCCGCTCATGAAAATCAAACCGAGGTGGC 300
OY	450 GAGCTTCGACACTGTGTCCCGCAGCGGCTTTACCTGGCGCTTC 492       Db       301 GAGCTTCGACACTGTGTCCCGCAGCGGCTTTACCTGGCGCTTC 343
RESULT 12	
A1828089/c	687 bp      mRNA      EST      21-DEC-1999
LOCUS	wk31f07.x1 NCI_CGAP.Brnz5 Homo sapiens cdna clone IMAGE:2413957 3'
DEFINITION	similar to SW:EPBZ_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR ; mRNA sequence.
ACCESSION	A1828089
VERSION	A1828089.1 GI:5448760
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 687) NCBI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BNGAP), Tumor Gene Index Unpublished (1998)
JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapst-email@nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D.





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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP  
Brazil

BASE COUNT	111 a	149 c	112 g	73 t
ORIGIN				

Query Match	9.0%;	Score 268;	DB 171;	Length 445;
Best Local Similarity	99.5%;	Pred. No. 9.8e-135;		
Matches 368;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

RESULT	15				
BF766632/c					
LOCUS	BF766632	440 bp	mrna	EST	12-JAN-2001
DEFINITION	IL2-CS0048-221100-245-El0	CS0048	Homo sapiens	CDNA, mRNA	sequence
ACCESSION	BF766632				
VERSION	BF766632.1	GI:12114532			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

**REFERENCE**  
AUTHORS

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidei: Homo.  
1 (bases 1 to 440)

Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M. F.

BASE COUNT	93 a	129 c	117 g	101 t
ORIGIN				

Query Match	7.5%	Score 221;	DB 169;	Length 440;
Best Local Similarity	99.28;	Pred. NO. 5e-109;		
Matches 371; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Wed Jul 11 10:25:34 2001

us-09-378-759-10.011.rst

Page 12

QY 1927 TACCGGAGAGCA 1940  
|||||  
Db 80 TACCGGAGAGCA 67

Search completed: July 10, 2001, 20:11:58  
Job time: 5870 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 16:01:53 ; Search time 2160.18 Seconds  
(without alignments)  
12961.583 Million cell updates/sec

Title: US-09-378-759-10  
Perfect score: 2962  
Sequence: 1 CCGCGCGCGCGCGTGGAAGA.....CCAAGCGCGCGCGCGCTCTGC 2962

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756.8	22.6	787	AU119907	AU119907 AU119907
2	657.4	22.2	192	AK017630	Mus muscu
3	639.6	21.6	153	BG425170	BG425170 602446663
4	613.2	20.7	769	BE314746	BE314746 601148809
5	600.8	20.3	705	AU133859	AU133859 AU133859
6	600.6	20.3	939	BF306234	BF306234 601833088
7	558.4	18.9	588	AM806532	AM806532 IL0-CT000
8	532.4	18.0	693	AI940384	AI940384 CM2-CT004
9	527.4	17.8	833	AU133418	AU133418 AU133418
10	525	17.7	970	AL552477	AL552477 AL552477
11	511.2	17.3	903	AL554027	AL554027 AL554027
12	507.4	17.1	517	AW938783	AW938783 PM3-DT006
13	499.8	16.9	912	AL547693	AL547693 AL547693
14	499	16.8	523	BE256685	BE256685 601107774
15	485	16.4	758	AM062316	AM062316 IL0-CT000
16	483.4	16.3	654	BE902753	BE902753 BE902753
17	480.2	16.2	552	AV607557	AV607557 AV607557
18	466.6	15.8	996	BE615780	BE615780 601279947
19	464.4	15.7	507	BF441135	BF441135 257290 MA
20	450	15.2	831	AL554205	AL554205 AL554205
21	442.2	14.9	932	BE906826	BE906826 601498394
22	441.4	14.9	921	BG171180	BG171180 602324261
23	440.8	14.9	448	AM845008	AM845008 RC0-CT000
24	440.6	14.9	779	BE531301	BE531301 601278227
25	439.2	14.8	887	BG117473	BG117473 602347490
26	437	14.8	813	AL529103	AL529103 AL529103
27	433.6	14.6	1001	CNS0316N	AL249080 Tetradon
28	425.2	14.4	804	BE285503	BE285503 601096865
29	424.4	14.3	787	BG481991	BG481991 602527834
30	415.6	14.0	445	BF945576	BF945576 CM1-NN019
31	408.2	13.8	951	BE272154	BE272154 601141236
32	407.2	13.7	888	BG033034	BG033034 602300142
33	403.6	13.6	672	BG253705	BG253705 602366763
34	401.6	13.5	904	BG179940	BG179940 602328973
35	400	13.5	1040	CNS0411L	AL293386 Tetradon
36	390.8	13.2	570	BF725165	BF725165 bx12n08.Y
37	390	13.2	901	BF122507	BF122507 601761507
38	389.6	13.2	968	BE371782	BE371782 601217768
39	388.4	13.1	793	BF136721	BF136721 601780488
40	385.8	13.0	558	BE754521	BE754521 208060 MA
41	384	13.0	440	BF766632	BF766632 IL2-CS004
42	383.2	12.9	862	BE615609	BE615609 601278614
43	380.4	12.8	580	AV595264	AV595264 AV595264
44	380.2	12.8	911	BE616843	BE616843 601280066
45	375	12.7	526	BF736600	BF736600 QV3-KT001

## ALIGNMENTS

RESULT	1	787 bp	19-OCT-2000
LOCUS	AU119907	787 bp	19-OCT-2000
DEFINITION	AU119907 HEMBA1 Homo sapiens cDNA clone HEMBA1006901 5', mRNA		
ACCESSION	AU119907		
VERSION	AU119907.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,		
	Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and		
	Isogai, T.		
TITLE	HRI human cDNA project		

## JOURNAL COMMENT

Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix  
Research Institute; cDNA library construction; Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

## FEATURES

source  
1. 787  
/organism="Homo sapiens"  
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/clone="HEMBA1006901"  
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/dev\_stage="embryo, 10 weeks"  
/note="Vector: pME18SFL3"

BASE COUNT 185 a 223 c 222 g 154 t 3 others  
ORIGIN

Query Match 25.6% Score 756.8; DB 107; Length 787;  
Best Local Similarity 99.1% Pred. No. 6.9e-171;  
Matches 780; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1700 ACTACACGAGGCGGCACATACCCCGAGCATGAGATCTACATGCTTCTACCTACG 1759  
1 ACTACACGAGGCGGCACATACCCCGAGCATGAGATCTACATGCTTCTACCTACG 60  
DB  
QY 1760 AGGACCCACGAGGCGGCAGTGGGAGTTGGCCAGGAATTTGACATCTCTGTCAAAA 1819  
AGGACCCACGAGGCGGCAGTGGGAGTTGGCCAGGAATTTGACATCTCTGTGTCAAAA 120  
DB  
QY 1820 TTGACGAGGTGATCGGAGCAGGAGGAGTTGGCGAGGTTCTGACATGCTTCAAGCTGC 1879  
TTGACGAGGTGATCGGAGCAGGAGGAGTTGGCGAGGTTCTGACATGCTTCAAGCTGC 180  
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QY 1880 CAGGCAAGAGAGATCTTTGGGCTCATGAGAGCTCAAGTGGGCTTCAAGAGAGC 1939  
CAGGCAAGAGAGATCTTTGGGCTCATGAGAGCTCAAGTGGGCTTCAAGAGAGC 240  
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QY 1940 AGCGCGGAGCTTCTGAGCGAAGCTTCATGAGGCGAGTTGCAACATCCCAAGTCA 1999  
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DB  
QY 2000 TCCACCTGAGGAGTGTCTGAGCAAGAGCAGCTGTATGATCATACCGAGTTCATGG 2059  
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QY 2060 AGAATGGCTCCCTGAGCTCTTCTCCGCAAAAGATGGGAGTTCAGATCCAGC 2119  
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QY 361 AGAATGGCTCCCTGAGCTCTTCTCCGCAAAAGATGGGAGTTCAGATCCAGC 420  
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Query Match	21.6%	Score 639.6	DB 153	Length 916
Best Local Similarity	96.2%	Pred. No. 9, 2e-143		
Match 731: Conservative	0	Mismatches 19	Indels 10	Gaps 7
QY 1484 GCACGTGTGGCAGGCTACGGGGCGCTACAGCGGCAAGATGTACTTCCAGACCATACAGAAAG 1543				
Ddb 2 GCACGCTGGCAGGCTACGGGGCGCTACAGCGGCAAGATGTACTTCCAGACCATACAGAAAG 61				
QY 1544 CCGAGTACCAGACAAAGCATCCAGAGAAAGTTGGCCACTCATCATCGCTCTCGGGCGCTG 1603				
Ddb 62 CCGAGTACCAGACAAAGCATCCAGAGAAAGTTGGCCACTCATCATCGCTCTCGGGCGCTG 121				
QY 1604 GCGTGGTCTTCCATCTCACTGTGTGTGTGCATCGGCATCGTGTGTATACAGACGGGGGTTTG 1663				
Ddb 122 GCGTGGTCTTCCATCTCACTGTGTGTGTGCATCGGCATCGTGTGTATACAGACGGGGGTTTG 181				
QY 1664 AGCGTGTCTACTCGAGATACAGGACAAAGCTGTCAACACTACACAGTGGCCACATATACC 1723				
Ddb 182 AGCGTGTCTACTCGAGATACAGGACAAAGCTGTCAACACTACACAGTGGCCACATATACC 241				
QY 1724 CAGGATGGAAGATCTACATCTCTTCCACTTCAGAGAGACCCCAAGAGGCACTGCGG 1783				
Ddb 242 CAGGATGGAAGATCTACATCTCTTCCACTTCAGAGAGACCCCAAGAGGCACTGCGG 301				
QY 1784 AGTTTGGCCAAAGAAATTGACATCTCTGTGTCAAAATTGACAGGTGATCGGACAGGG 1843				
Ddb 302 AGTTTGGCCAAAGAAATTGACATCTCTGTGTCAAAATTGACAGGTGATCGGACAGGG 361				
QY 1844 AGTTTGGCCAGGTCTGCATATGGGCGCACTCGAAGTCCAGAGGCAAGAGAGATCTTTGTGG 1903				
Ddb 362 AG-TTGGCCAGGTCTGCATATGGGCGCACTCGAAGTCCAGAGGCAAGAGAGATCTTTGTGG 420				
QY 1904 CCATCAAGACGCTCAAGTGTGGGCTACACAGGAGAAACAGCGCGGGACTTCTCTGAGCGAAG 1963				
Ddb 421 CCATCAAGACGCTCAAGTGTGGGCTACACAGGAGAAACAGCGCGGGACTTCTCTGAGCGAAG 480				
QY 1964 CCTTCATCATGGGCGCAGTTTCGACATCCCAAGTGCATCCACTGAGGGGTGTGAGACCA 2023				
Ddb 481 CCTTCATCATGGGCGCAGTTTCGACATCCCAAGTGCATCCACTGAGGGGTGTGAGACCA 540				
QY 2024 AGAGCACCCTGTGATGATCATCACCGAGTTCATGGAGAAATGGCTCCCTGGACACTCTTTC 2083				
Ddb 541 AGAGCACCCTGTGATGATCATCACCGAGTTCATGGAGAAATGGCTCCCTGGAACTCTTTC 600				
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Ddb 601 TCCGGGCAAAAGCATGGGCGAGTTTACAGATCATTCAGCTGTGGGAGTCTTC-GGGGCAAT 660				
QY 2142 CGCAGCT--GGCATGGAAGTACTCTGG--CAGACATGAACATATGT--CACCGTAGCCTGGCT 2196				
Ddb 661 CGCAGCTTGGCATGGAAGTACTCTGGGCGAGGACATGAAATATGTTCACCGGTGAATCGGCT 720				
QY 2197 GCCCGCAACATCTCTGTCAACAGCAACCTGTGTGCAAG 2236				
Ddb 721 GCC--GAAAAATACTCGTCAACAGCAACCTGTGTGCAAG 758				
RESULT 4				
BE314746	769 bp	mrna	EST	26-OCT-2000
LOCUS	601148809F1 NIH_MGC_19	Homo sapiens cDNA clone IMAGE:3501578 5'		
DEFINITION	mRNA sequence.			
ACCESSION	BE314746			
VERSION	BE314746.1	GI:9136248		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	NIH-MGC http://mgs.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

Plate: L10M172 row: a column: 03

High quality sequence start: 16

High quality sequence stop: 683.

## FEATURES

source

Location/Qualifiers

1..769

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3501578"

/clone\_lib="NIH\_MGC\_19"

/tissue\_type="neuroblastoma"

/lab\_host="DH10B (phage-resistant)"

/note="organ: brain; Vector: pOTB; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGCG. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 162 a 254 c 214 g 139 t

ORIGIN

Query Match

Best Local Similarity 20.7%; Score 613.2; DB 166; Length 769;  
Matches 658; Conservative 0; Pred. No. 1.9e-136;

Mismatches 33; Indels 5; Gaps 2;

661 GTACCCATCAAGCTCTACTGTACGAGGAGGCGGCG---AGTGGCTGTGGCCATCGGCGG 716

21 GTACCCATCAAGCTCTACTGTACGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 80

717 CTGATGTGCAAGAGGCTTCCAGGCGGCTTGAGATGCGACCGCTGCGGAGGTTGTC 776

81 CTGATGTGCAAGAGGCTTCCAGGCGGCTTGAGATGCGACCGCTGCGGAGGTTGTC 140

777 ATCTGGACTTTCAAGGCGCAACCAAGGGGAGGCGCTGTACCCACTGTCTCCATCAACAG 836

141 ATCTGGACTTTCAAGGCGCAACCAAGGGGAGGCGCTGTACCCACTGTCTCCATCAACAG 200

837 CCGGACCACTTGTGAAGGGCGCAACTGTGTCTGCCGCAATGGCTACTACAGACAGA 896

201 CCGGACCACTTGTGAAGGGCGCAACTGTGTCTGCCGCAATGGCTACTACAGACAGA 260

897 CCGGACCACTTGTGAAGGGCGCAACTGTGTCTGCCGCAATGGCTACTACAGACAGA 956

261 CCGGACCACTTGTGAAGGGCGCAACTGTGTCTGCCGCAATGGCTACTACAGACAGA 320

957 CAGTGTCAATGAGACCTCCCTCATGTGTGAGTGACCCCTCCCGGAGCTCGGGA-GGCC 1015

321 CAGTGTCAATGAGACCTCCCTCATGTGTGAGTGACCCCTCCCGGAGCTCGGGA-GGCC 380

1016 GAGAGAGCTCTGTCAACATCATGTGCAAGAGCTGTGGCTGGGCGGGGTGCTGCA 1075

381 GAGAGAGCTCTGTCAACATCATGTGCAAGAGCTGTGGCTGGGCGGGGTGCTGCA 440

1076 CCGGCTGGGGGAGCATATGAGTAGAGTACGAGCAGGAGTACAGGCTGACCGAGCAGCA 1135

441 CCGGCTGGGGGAGCATATGAGTAGAGTACGAGCAGGAGTACAGGCTGACCGAGCAGCA 500

1136 TTATACATGAGTACCTGTGGCCACACACCACTACAGCTTCAGATCCAGAGGTGGAAG 1195

501 TTATACATGAGTACCTGTGGCCACACACCACTACAGCTTCAGATCCAGAGGTGGAAG 560

1196 GGGTACTAGCAGAGCCCTTCTGCTGAGTGTGCTGTGGAATCACCACCAACC 1255

Db 561 GCGTACTGACACAGAGCCCTTCTGCGCTCAGTTCGCCCTGTGTGACATCACCACCAAGC 620

Qy 1256 AGGAGCTCCATCGGCGAGTGTTCATCATCATGATGAGTACCCCGGAGGAGCATTTA 1315

Db 621 AGGAGCTCCATCGGCGAGTGTTCATCATCATGATGAGTACCCCGGAGGAGCATTTA 680

Qy 1316 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1351

Db 681 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 716

RESULT 5

AU133859 705 bp mRNA EST 24-OCT-2000

LOCUS AU133859 OVARC1 Homo sapiens cDNA clone OVARC1000793 5', mRNA

DEFINITION sequence.

ACCESSION AU133859 GI:10994398

VERSION AU133859

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 705)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

HRI human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-32-3951

Fax: 81-438-32-3952

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix

Research Institute; cDNA library construction; Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

1..705

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="OVARC1000793"

/clone\_lib="OVARC1"

/tissue\_type="ovary, tumor tissue"

/note="Vector: pHEB5F13"

BASE COUNT 176 a 199 c 199 g 128 t 3 others

ORIGIN

Query Match 20.3%; Score 600.8; DB 108; Length 705;

Best Local Similarity 97.9%; Pred. No. 1.9e-133;

Matches 621; Conservative 0; Mismatches 7; Indels 6; Gaps 1;

Qy 1243 ATCAACACCAACAGGAGCTTCATCGGAGTGTTCATCATCATGATGAGGAGCGGAGC 1302

Db 4 ATCAACACCAACAGGAGCTTCATCGGAGTGTTCATCATCATGATGAGGAGCGGAGC 63

Qy 1303 GTGAGACGATTAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1362

Db 64 GTGAGACGATTAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 123

Qy 1363 TATGAGCTGAGTACTATGAGAAGAGAGCTAGTAGTACCAAGCCACAGCCATTTAAAGC 1422

Db 124 TATGAGCTGAGTACTATGAGAAGAGAGCTAGTAGTACCAAGCCACAGCCATTTAAAGC 183

Qy 1423 CCGACCAACAGGCTAC-----GGGCTCAAAAGCCGGGCGCATTTATGCTTCCAGGTTG 1476

Db 184 CCGACCAACAGGCTACCGGTGAGAGGCGCTCAAAAGCCGGGCGCATTTATGCTTCCAGGTTG 243

Qy 1477 CCGGACGACGACTGTGAGGCTACAGGCGGCTACAGGCGGCAAGATGTACTTCCAGACCATG 1536



	Query Match	20.3%	Score 600.6;	Df 147;	Length 939;	
	Best Local Similarity	95.1%	Pred.	No.2,1e-133;		
	Matches 674;	Conservative	0;	Mismatches 29;	Indels 6;	Gaps 5;
OY	36	CACATACGACACACTGTAGAGCTGGGCGTGGATGGTCATCCTCCATCAGGGTGGAAGAGT	95			
Db	2	CACATACGACGACACTGTAGAGCTGGGCGTGGATGGTCATCCTCCATCAGGGTGGAAGAGT	61			
OY	96	GAGTGGCTACGATGAGAACAATGAACACGATCCGCAGCTACCAGGTGTGCCAACGTGTTGA	155			
Db	62	GAGTGGCTACGATGAGAACAATGAACACGATCCGCAGCTACCAGGTGTGCCAACGTGTTGA	121			
OY	156	GTCGAAGCCAGAACAAACGCGCTACGAGCAAGATTATATCCGGCGCGTGGGCCAACCAGT	215			
Db	122	GTCGAAGCCAGAACAAACGCGCTACGAGCAAGATTATATCCGGCGCGTGGGCCAACCAGT	181			
OY	216	CCACGTGGAGATGAAGTTTTTCGCTGCTGACTGACGACGATCCCAAGCGTGCCTGCCTC	275			
Db	182	CCACGTGGAGATGAAGTTTTTCGCTGCTGACTGACGACGATCCCAAGCGTGCCTGCCTC	241			
OY	276	CTCGAAGSAGACCTTCAACCTCTATTACTATGAGSGCTGACCTTAGCTGCGGC -CACCAAGA	334			
Db	242	CTCGAAGSAGACCTTCAACCTCTATTACTATGAGSGCTGACCTTAGCTGCGGCACCAAGA	301			
OY	335	CCCTTCCCCCACTGGATGGAGAAATCATAGGCTGGAAGGTGGATATACATTGACCCGACGAGA	394			
Db	302	CCCTTCCCCCACTGGATGGAGAAATCATAGGCTGGAAGGTGGATATACATTGACCCGACGAGA	361			
OY	395	GCTTCTCTCCACAGTGGACCTGGGTGGCGCGCTCATGATAAATCAACACGAGGTGCGGAGCT	454			
Db	362	GCTTCTCTCCACAGTGGACCTGGGTGGCGCGCTCATGATAAATCAACACGAGGTGCGGAGCT	421			
OY	455	TGCGACCTGTGTCCCAGAGCGGGCTTCTACCGTGGGCTTCCAGAGCATATGGCGGCTGCATGT	514			
Db	422	TGCGACCTGTGTCCCAGAGCGGGCTTCTACCGTGGGCTTCCAGAGCATATGGCGG--TGATGT	479			
OY	515	CCCTCATCGCCGTCGCTGCTCTTCTACCGCAAGTGGCCCCCGCATCTCCAGATATGGCGCCA	574			
Db	480	CCCTCATCGCCGTCGCTGCTCTTCTACCGCAAGTGGCCCCCGCATCTCCAGATATGGCGC-CA	538			
OY	575	TCTTTCACAGAAAACCTGTGCGGGGCTGAGAGCACATCCCTGTGTGGCTGCCCGGGGACACT	634			
Db	539	TCTTTCACAGAAAACCTGTGCGGGGCTGAGAGCACATCCCTGTGTGGCTGCCCGGGGACAGT	598			
OY	635	GCAATCGCCCAATGGCGAAGAGGTGATGATACCATTAACCTCTACTGTAAACGGGAGACGGCG	694			
Db	599	GGATCG-CAAATGCGGAABAAGGTGATGTATACCATTAACAGCTCTACTGTAAACGGGAGACGGC	657			
OY	695	AGTGCGCTGTGCGCCATTCGGGCGCTGCATGTGCCAAGCAGGCTTGCAGGC 743				
Db	658	GAAAGGTGTGTG-CCATCGGGCGCGCTGATGGCAAAGCAGGCTGCMAAGAC 705				
RESULT						
LOCUS	AW806532/c	588 bp	mRNA	EST	17-MAY-2000	
DEFINITION	ILD-ST0002-160599-012 ST0002 Homo sapiens cDNA, mRNA sequence.					
ACCESSION	AW806532					
VERSION	AW806532.1	GI:7899531				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hominidae; Homo.					
REFERENCE						
AUTHORS	Nagas Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Diagel,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bais,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,L.R.R., Reis,L.F., de Souza,S.J. and Simpson,A.U.J. Shotgun sequencing of the human transcriptome with ORF expressed					

JOURNAL  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE  
20202663  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2=IL0-ST0002-160  
599-012&t3=1999-05-16&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 589.

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/clone\_lib="ST0002"  
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/note="Organ: stomach; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196/716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
Location/Qualifiers  
1. 588  
/db\_xref="taxon:9606"  
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/dev\_stage="Adult"  
/note="Organ: stomach; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196/716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
Location/Qualifiers

BASE COUNT  
111 a 152 c 192 g 133 t

Query Match  
Best Local Similarity 18.9%; Score 558.4; DB 120; Length 588;  
Matches 577; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

2070 CCTGAGACTCTTTCTCCGCAAAAAGCATGGGAGTTCACAGTATCCAGCTGGTGGGCAT 2129  
|||||  
588 CCTGAGACTCTTTCTCCGCAAAAAGCATGGGAGTTCACAGTATCCAGCTGGTGGGCAT 531  
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2130 GCTTCGGGGGATGGAGCTGGGATGAAGTACCTGGGAGAGATGATATATTTACCGTGA 2189  
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530 GCTTCGGGGGATGGAGCTGGGATGAAGTACCTGGGAGAGATGATATATTTACCGTGA 471  
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2190 CCTGGCTGGCCGCAACATCTCTGTCACAGCAAGCACTGTGTGCAAGTGTGCGACTTTGG 2249  
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470 CCTGGCTGGCCGCAACATCTCTGTCACAGCAAGCACTGTGTGCAAGTGTGCGACTTTGG 411  
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2250 GCTCTCAGCTTTCTAGAGAGCATACCTCAGACCCACCCTACAGATGCGCTGGGCGG 2309  
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410 GCTCTCAGCTTTCTAGAGAGCATACCTCAGACCCACCCTACAGATGCGCTGGGCGG 351  
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2310 AAGATTCCTCCATCGCTGGAGACCCCGGAAGCATCCAGTACCGGAGTTCACCTCGGC 2369  
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350 AAGATTCCTCCATCGCTGGAGACCCCGGAAGCATCCAGTACCGGAGTTCACCTCGGC 291  
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2370 CAGTATGTGTGAGCTACGGCATTGTCAATGTGGAGGTGATGTCTTATGGGAGCGGCC 2429  
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290 CAGTATGTGTGAGCTACGGCATTGTCAATGTGGAGGTGATGTCTTATGGGAGCGGCC 231  
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2430 CTACTGGGACATGACCAACAGAGATGATATCAATGATGAGAGGAGTATTCGGCTGCC 2489  
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230 CTACTGGGACATGACCAACAGAGATGATATCAATGATGAGAGGAGTATTCGGCTGCC 171  
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2490 ACCGGCCATGAGTGGCCGAGGCGCTGACCAACATCATGTGAGACTGTTGGCAGAGA 2549  
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170 ACCGGCCATGAGTGGCCGAGGCGCTGACCAACATCATGTGAGACTGTTGGCAGAGA 111  
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2550 CCGCAACACACCGGCGCAAGTGTGGCCAAATTTGTCAACACGCTAGACAGATATCCGCA 2609  
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110 CCGCAACACACCGGCGCAAGTGTGGCCAAATTTGTCAACACGCTAGACAGATATCCGCA 51  
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QY 2610 TCCCAACAGCTCAAAAGCATGGGCGCCCTCTCTCTGCGATCAACCTGC 2659  
Db 50 TCCCAACAGCTCAAAAGCATGGGCGCCCTCTCTCTGCGATCAACCTGC 1

RESULT 8  
AI940384/c 693 bp mRNA EST 03-AUG-1999  
LOCUS  
DEFINITION  
CM2-CT0040-300799-002-h10 CT0040 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
AI940384  
VERSION  
AI940384.1 GI:5687365  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2=CM2-CT0040-  
300799-002-h10&t3=1999-07-30&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 39  
High quality sequence stop: 692.  
Location/Qualifiers

FEATURES  
Source  
1. 693  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0040"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
/716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
Location/Qualifiers

BASE COUNT  
141 a 178 c 210 g 162 t 2 others

Query Match  
Best Local Similarity 18.0%; Score 532.4; DB 104; Length 693;  
Matches 561; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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591 GGCAGTTCACAGTATCCAGCTGTGGGATGCTTCGGGATGCGACCTGGATGAAGT 533  
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2159 ACCTGGCAGACATGATGATGTTACCGCTGACCTGGTCCCGCAACATCTCGTCAACA 2218  
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532 ACCTGGCAGACATGATGATGTTACCGCTGACCTGGTCCCGCAACATCTCGTCAACA 473  
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2219 GCAACCTGGTTCGAAGGTGCGGACTTTGGGCTCTCAGCTTTCTAGAGAGATGAT 2278  
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472 GCAACCTGGTTCGAAGGTGCGGACTTTGGGCTCTCAGCTTTCTAGAGAGATGAT 413  
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2279 CAGACCCACCTACACGAGTCCCTGGGCGGAAGTTCCCATCCGCTGAGACACCCCGG 2338  
|||||  
412 CAGACCCACCTACACGAGTCCCTGGGCGGAAGTTCCCATCCGCTGAGACACCCCGG 353  
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QY 2339 AAGCATCTACCTACCGAAGTTCACTCGGCCAGTGTGTGAGCTACGCGCATTTGTCA 2398  
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DB 352 NAGCCATCAGTACCGGATTTTACGTGCGCCAGTGTGTGAGCTACGCGCATTTGTCA 293  
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QY 2399 TGTGGAGGTGATGCTTATGTTGGGAGCGCCCTACTGGACATGACCAACGAGATGTAA 2458  
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DB 292 TGTGGAGGTGATGCTTATGTTGGGAGCGCCCTACTGGACATGACCAACGAGATGTAA 233  
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QY 2459 TCAATGCCATTTGAGGAGTATGCTGCGCCAGCCCATGGATGAGCCGAGCGCCCTGC 2518  
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DB 232 TCAATGCCATTTGAGGAGTATGCTGCGCCAGCCCATGGATGAGCCGAGCGCCCTGC 173  
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QY 2519 ACCAATCATGCTGAGTCTTTGGGAGAGAGACCGGACCGCCCAAGTTGGCCCAA 2578  
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DB 172 ACCAATCATGCTGAGTCTTTGGGAGAGAGACCGGACCGCCCAAGTTGGCCCAA 113  
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QY 2579 TTGTCAACAGCTGATGATGATCCCAATCCCAAGCTTCAAGCATGGGCGCC 2638  
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DB 112 -TGTCAACAGCTGATGATGATCCCAATCCCAAGCTTCAAGCATGGGCGCC 54  
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QY 2639 TCTCTGTGCTCAACCTGCGCTGTGAGCCG 2673  
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DB 53 TCTCTGTGCTCAACCTGCGCTGTGAGATGC 19  
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## RESULT 9

AUI33418 833 bp mRNA EST 24-OCT-2000  
LOCUS AUI33418 NT2RP4 Homo sapiens cDNA clone NT2RP4002019 5', mRNA  
DEFINITION  
ACCESSION AUI33418  
VERSION AUI33418.1 GI:1093957  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 833)  
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J.,  
Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuno, Y., and  
Isogai, T.

## TITLE

HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,  
Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T., Sugano,  
S., Masuno, Y., Isogai, T.)

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kiserazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952

Email: genomics@hri.co.jp  
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

## FEATURES

Location/Qualifiers  
1..833

BASE COUNT 176 a 237 c 251 g 164 t 5 others  
ORIGIN  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NT2RP4002019"  
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/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor  
cells after 2-weeks retinoic acid (RA) induction"

Query Match 17.8%; Score 527.4; DB 108; Length 833;  
Best local similarity 79.3%; Pred. No. 7, 4e-116;  
Matches 660; Conservative 0; Mismatches 166; Indels 6; Gaps 3;

QY 1805 TCTCTGTGTCAAAATTGACAGTGTATCGAGCAAGGAGATTGGGAGGTCTGCAGTG 1864  
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DB 4 TCTCTAGTTCAGATTTGAGAGAGTGTATGGTGCAGGTGATTTGGGAGGTCTGCAGTG 63  
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QY 1865 GCCACCTGAACCTGCCAGGAGAGAGATCTTTGGGACATCAAGACGCTCAAGTCGG 1924  
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DB 64 GCGGCTCAAGGCCCCAGGAGAGAGAGAGAGTGTGTGGCAATCAAGACCTGAAAGGTG 123  
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QY 1925 GCTACAGAGAGAGAGAGAGGCGGGAGCTTCTGAGCAGAGCTTCATGAGGCGCATTTG 1984  
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DB 124 GCTACAGAGAGAGAGAGGCGGGAGTGTGTGTGAGAGAGGCTTCATGATGAGGCGCATTTG 183  
|||||  
QY 1985 ACCATCCCAAGCTATCCACTGGAAGGTGTGTGACCAAGACACACTGTGATGATCA 2044  
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DB 184 AGCACCCCAATATATCCGCTGGAGGCGCTGTGTCCACCAACAGATGCGCCGTGATGATTC 243  
|||||  
QY 2045 TCACGAGTTGATGAGAGAGATGCTCCCGGAGCTCTTCTCCGCGCAAAAGATGGGAGT 2104  
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DB 244 TCACGAGTTGATGAGAGAGAGAGAGGCGCGCTGTGAGTCTTCTCCGCGTAAACAGAGAGT 303  
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QY 2105 TCACGATCATCAGCTGTGAGGATGCTTCCGAGGATGAGCAGTGTGAGTGAATGATG 2164  
|||||  
DB 304 TCACGATCATCAGCTGTGAGGATGCTTCCGAGGATGAGCAGTGTGAGTGAATGATG 363  
|||||  
QY 2165 CAGACATCACTATGTTTACCGTACCTGCGTCCCGCAACATCTCTCAACAGCAAC 2224  
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DB 364 CCGAGATAGAGTACCTCCACGAGACCTGTGCTGTGCAACATCTTACTACACAGCAAC 423  
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QY 2225 TGTGTGCAAGGTGTGAGCTTTGGGCTCTGACGCTTCTGAGAGAGCATCTTCAGAC 2284  
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DB 424 TGTGTGCAAGGTGTGAGCTTTGGGCTCTGACGCTTCTGAGAGAGCATCTTCAGAC 483  
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QY 2285 CCACCTACACAGTCCCTGGGCGGAGAAAGTTCCCATCCGCTGACACCGCCGAGCA 2344  
|||||  
DB 484 CCACCTACACAGTCCCTGGGCGGAGAAAGTTCCCATCCGCTGACACCGCCGAGCA 543  
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QY 2345 TCCACTACCGGAGTTCACCTCGGCGGAGATGTTGGAGTACGAGCAATTTGATGATGG 2404  
|||||  
DB 544 TGTGCTTCGAGAGTTCACCTTCGCGAGTATGCTTGGAGTTACGAGTGTGATGATGG 603  
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QY 2405 AGGTATGCTCTATGGGAGGAGCGCCCTACTGTGGACATGCCAACCAGATGTAATCAATG 2464  
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DB 782 TCAAGGCGCCCTGACAGAGAGATCCGGAACCGCGNACAGTNAATATGCTGG 833  
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LOCUS AL552477 LTI.NFL006.PL2 Homo sapiens cDNA clone CS0D1070YA06 5  
DEFINITION  
ACCESSION AL552477  
VERSION AL552477.1 GI:12891411  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 970)  
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization

[illegible]

QY 2003 .

\_\_\_\_\_

```

FEATURES      Location/qualifiers
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CT  
DB

13 GNCGIGHGIIICIGAGCGAGGCLCCCHICHIIGGGCCAGTTCGAGCACCCTCA

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Db 75 GCCTGGAGGGCGGTGTCACCAACAGATGCCGTCATCTCTCACAAGTTTCATGGAGA 134

Qy 2063 ATGGCTCCCTGGACTCCTCTTCTCCGGCAAAAGCA-TGGGCAATTTCACAGTCACTCAGCTG 2121

Db 135 ACGACGCCCTGGAGCTCCTCTGGGGCTAAAGACAGACAGATTTCACAGTCACTCAGCTC 194

Qy 2122 GTGGGCAATGCTTCGGGGCATGCGACAGTGAAGTACCTGGACAGACATCATATGTT 2181

Db 195 GTGGGCAATGCTTCGGGGCATGCGACAGTGAAGTACCTGGACAGACATCATATGTT 254

Qy 2182 CACGGTGCCTGGGTCGGGCAACATCTCTGCAACACACACCTGGTGGAGGTGCG 2241

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Qy 2301 CCTGGGCGAAAGTTCCCATTCCTGTCAGACAGCCCGGAGACCATTCAGTCCGAGATT 2360

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Qy 2361 CACCTCGGCGAGATGATGATGAGTACGGGATGTCATGTCGAGAGATGATGCTCTATGG 2420

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Qy 2481 TCGGCTGCCACCGCCCATGAGACTGCCGAGCGCTGCAACCACTCATGTCGAGCTGTTG 2540

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Qy 2541 GCAGAAAGACGCGCAACACCGGCGCAAGTGGGCAAAATGTCACAGCTGACAGAT 2600

Db 614 GCAGAAAGACGCGCAAGTGGGCGCAAGTGGGCGCAAGTGGGCGCAAGTGGGCGCAAGT 673

Qy 2601 GATCGGCAATCCCAACAGCTCAAAAGCCATGCGGCGCTCTCTCTGTCATGATCACTGCGC 2660

Db 674 GATCGGCAATCCCGGCGCAAGCTCAAAATGTCGCGCGGAGATGCGGCGCTCTCAACGCC 733

Qy 2661 GCTGCTGAGCGACAGATGCTCCGAGTACACAGCTTTAAACAGGTGAGAGAGTGCCTGGA 2720

Db 734 TCTCTGAGCGACGCGAGCTCACTACAGCTTTGGCTGTGGGCGAGTGCCTGCG 793

Qy 2721 GGCATCAAGATGAGGCGAGTACAAAGAGAGCTTGGCAATGCGGCGCTTCACTCTTGA 2780

Db 794 GGCATCAAGATGAGGCGAGTACAAAGATGAGGCGAGTACAAAGATGAGGCGCTTGA 853

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RESULT 12  
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 DEFINITION  
 ACCESSION AM938783  
 VERSION AM938783.1 GI:8114229  
 KEYWORDS EST.

SOURCE  
 ORGANISM

human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS 1 (bases 1 to 517)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

FEATURES  
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 Site:2: Smat; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent Application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 97 a 133 c 168 g 119 t  
 ORIGIN

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Db 517 TCGCAGTGGGCTGAGAGTACGTCGACAGATGATGTCACCGTGCCTGCGCC 458

Qy 2201 GCACATCTCTGTCACAGCAACGTCGTCTGCAAGGTGTCGAGCTTCTCAGCT 2260

Db 457 GCACATCTCTGTCACAGCAACGTCGTCTGCAAGGTGTCGAGCTTCTCAGCT 398

Qy 2261 TTCTAGAGAGCATACCTCAGACCCCATACACAGTGCCTGGGCGGAAGTCCCA 2320

Db 397 TTCTAGAGAGCATACCTCAGACCCCATACACAGTGCCTGGGCGGAAGTCCCA 338

Qy 2321 TCCGCTGACAGCCCGGAGGACATCAGTACCGGAAGTTCACCTCGGCACTGATGT 2380

Db 337 TCCGCTGACAGCCCGGAGGACATCAGTACCGGAAGTTCACCTCGGCACTGATGT 278

Qy 2381 GGAGCTACGGCATTTGTCATGTGAGAGTGATGTCCTATGAGGAGCGGCTTCTGAGACA 2440

Db 277 GGAGCTACGGCATTTGTCATGTGAGAGTGATGTCCTATGAGGAGCGGCTTCTGAGACA 218

Qy 2441 TCACCAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2500

Db 217 TCACCAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 158

Qy 2501 ACTGCCGAGCGCCCTGACCAACTCATGCTGAGCTGTTGGCAGAGACCGCAACACC 2560

Db 157 ACTGCCGAGCGCCCTGACCAACTCATGCTGAGCTGTTGGCAGAGACCGCAACACC 98

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Qy 2621 TCAGAGCATGAGCGGCGGCTCTCTGTCGATCACT 2657

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LOCUS AL547693 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS01017YL08 5  
DEFINITION prime, mRNA sequence.  
ACCESSION AL547693  
VERSION AL547693.1 GI:12881993  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 912)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
Source  
1. 912  
Location/Qualifiers  
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BASE COUNT 190 a 280 c 253 g 184 t 5 others  
ORIGIN

Query Match 16.9%; Score 499.8; DB 106; Length 912;  
Best Local Similarity 75.5%; Pred. No. 3.1e-109;  
Matches 680; Conservative 4; Mismatches 211; Indels 6; Gaps 5;

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Db 1 TCCATCATGGGCCAGTTCGACCATCCCAAGTCATCCACTGGAGGCTGCTGACCAAG 60  
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QY 2026 AGCACACTGTGATGATCAGCAGGATTCAGAGAAAGGCTCCGACCTCTTC 2085  
|||||  
Db 61 AGCATGCCCTCATGATTTTCACAGATTCATGAGAGAGCGCCCTGGACTCTTCCTG 120  
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QY 2086 CGGCAAAAGCATGGGAGTTCACAGTTCATCCAGTGGTGGCATGCTTCGGGATCGCA 2145  
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Db 121 CGGCTAAAGCAGGAGAGTTCACAGTTCATCCAGTGGTGGCATGCTTCGGGATCGCC 180  
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QY 2146 GCTGGCATGAAGTACCTGGCAGACATGAACTATGTTACCGTGACCTGGTCCCGCAAC 2205  
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QY 2206 ATCTGTGTAAGCAAGCAAGCTGTCGAAGTGTGCGACTTTGGGCTCTACGCTTTCTA 2265  
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Db 241 ATCTGTGTAAGCAAGCAAGCTGTCGAAGTGTGCGACTTTGGGCTCTACGCTTTCTG 300  
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Db 301 GAGGAGCATACCTCAGATCCACCTACACAGTGGCTGGGCGGAAGTTCCTCATCCG 360  
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QY 2326 TGGACAGCCCCGGAAGCATCCAGTACCGGAGTTCACCTGGGCGAGTGTGTGAGAG 2385  
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Db 361 TGGACTGCCCGGAGAGGCATTCGCTTCGGGAAGTTCATCTCCGCAATGATGCTGAGT 420  
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QY 2625 AGCCATGGCGCCCTCTCTCTGCAATCAACCTGCGCTGCTGACCGCATCCCGCA 2684  
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QY 2865 C 2865  
Db 896 C 896

RESULT 14  
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mRNA sequence.  
ACCESSION BE256685  
VERSION BE256685.1 GI:9127149  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgraphs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM129 row: d column: 20  
High quality sequence stop: 522.  
Location/Qualifiers  
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    in the laboratory of Gerald M. Rubin (University of
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    (Stratagene) and Superscript II RT (Life Technologies).
    Note: This is a NIH-MGC library."

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QY	894	AGACCTGGACCCCTTGGACATGCCCTGCACAA-CCATCCCTTCCTCCGGCCGCCAGCGTGTGA	952					
DB	61	AACACCTGGACCCCTTGGACATGCCCTGCACAACTCCATCCCTTCCTCCGGCCGCCAGCGTGTGA	120					
QY	953	TTTCCAGTGTCAATGAGA-CTTCCTCATGTGTGAGTGGACCCCTTCCCGCAGACTCCGGA	1011					

QY	1012	GGCGAGAGGACCTCGTCTCAACATCATCTGCAAGAGCTGTGGCTCGGGCGGGGTGCC	1071
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QY	1072	TGCACCCGCTCGGGGGAACAATGTACAGTACGCACCAAGCCAGCTAGGCTGACCGAGCCA	1131
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QY	1132	CGCATTTACATCACTGACGTGCGTGGGCCACACCCAGTACACCTTCCAGATCCAGGCTGTG	1191
Db	301	CGCATTTACATCACTGACGTGCGTGGGCCACACCCAGTACACCTTCCAGATCCAGGCTGTG	360
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Db	361	AACGGCGTTACTGTGACACGAGGCCCTTCTCGCTCAGTTCGCGCTGTGTGAACATCACACC	420
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VERSION	AM062316.1 GI:6013701
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 758)
AUTHORS	HCGP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a> .
TITLE	The FAPESP/LICR Human Cancer Genome Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

**FEATURES**

Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-IL0-CR0002-050>)  
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Location/Qualifiers

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from ORESPEC PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
166 a 189 c 236 g 167 t
BASE COUNT
ORIGIN

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OY	2145	AGCTGGCATGGAAGTACGCGGCGACATGAACATCTTACACCGTGACCTGGGCGCCGGCAA	2204			
Db	495	AGCTGGCATGGAAGTACGCGGCGACATGAACATCTTACACCGTGACCTGGGCGCCGGCAA	436			
OY	2205	CATCTCTGTCAACAGCAACCTGGTCTGCAAGGTGTGCGACCTTGTGGGCTCTACAGCTTCT	2264			
Db	435	CATCTCTGTCAACAGCAACCTGGTCTGCAAGGTGTGCGACCTTGTGGGCTCTACAGCTTCT	376			
OY	2265	AGAGGACCATATCTTAGACCCGACCTACACACAGTCCCTGGGCGGAAAGTTCCCATCG	2324			
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Db	315	CTGGACACGCCCCGGGAAGCGATTCAGTACCGGAAGTTCACTCGGGCATTTGATGTGTGAG	256			
OY	2385	CTAGCGCATTTGTATGTGGGAGGTGATGTCTATGGGAGGCGGCCCTACTGGGACATGAC	2444			
Db	255	CTAGCGCATTTGTATGTGGGAGGTGATGTCTATGGGAGGCGGCCCTACTGGGACATGAC	196			
OY	2445	CAACCGAGATGTAATCAATATGCGATTGGACAGGACATATGGGCTGGCCACCGCCCATGGACTG	2504			
Db	195	CAACCGAGATGTAATCAATATGCGATTGGACAGGACATATGGGCTGGCCACCGCCCATGGACTG	136			
OY	2505	CCCGAGGCGCCCTGCGACCAACTCATCTGGAGCTGTGGGAGAAAGAACCCCAACACCGGCC	2564			
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OY	2565	CAAGTTGGGCGCAAAATTGTCAACACGCTAGACAAAGATGATCCGCAATGCCCAACAGGCTCAA	2624			
Db	75	CAGGTTGCCCAAAATT-TCAACACGCTAGACAAAGATGATCCGCAATGCCCAACAGGCTCAA	17			
OY	2625	AGCCATGGCGGCC 2637				
Db	16	ACCTATGGGCCCC 4				

Wed Jul 11 10:25:42 2001

us-09-378-759-10.rst

Page 14

Search completed: July 10, 2001, 18:34:01  
Job time: 9128 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 20:12:03 ; Search time 120.21 Seconds

(Without alignments)  
7317.489 Million cell updates/sec

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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 392237 seqs, 148486726 residues

Word size : 0

Total number of hits satisfying chosen parameters: 784474

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	1.0	3836	5	US-09-560-875A-7981 Sequence 7981, App
2	23	0.8	399	5	US-09-872-850-298 Sequence 298, App
3	23	0.8	504	5	US-09-872-850-301 Sequence 301, App
4	23	0.8	2451	5	US-09-771-161A-4 Sequence 4, Appl
5	21	0.7	4016	5	US-09-560-875A-6907 Sequence 6907, App
6	19	0.5	382	5	US-09-693-692-967 Sequence 967, App
7	19	0.5	2083	1	PCR-US01-10485A-316 Sequence 316, App
8	19	0.5	5374	5	US-09-560-875A-7710 Sequence 7710, App
9	19	0.5	16350	5	US-09-793-706A-3 Sequence 3, Appl
10	18	0.6	207	4	US-08-221-623D-2326 Sequence 2326, App
11	18	0.6	327	5	US-09-371-146A-12431 Sequence 12431, A
12	18	0.6	487	5	US-09-649-165A-760 Sequence 760, App
13	18	0.6	525	5	US-09-371-146A-253158 Sequence 253158, A
14	18	0.6	109	5	US-09-237-183A-5 Sequence 5, Appl
15	17	0.6	128	5	US-09-237-183A-133 Sequence 133, App
16	17	0.6	149	5	US-09-872-850-5 Sequence 5, Appl
17	17	0.6	150	5	US-09-237-183A-134 Sequence 134, App
18	17	0.6	150	5	US-09-371-146A-69843 Sequence 69843, A
19	17	0.6	171	5	US-09-237-183A-127 Sequence 127, App
20	17	0.6	171	5	US-09-371-146A-66812 Sequence 66812, A
21	17	0.6	182	5	US-09-237-183A-82 Sequence 82, Appl
22	17	0.6	182	5	US-09-371-146A-42876 Sequence 42876, A
23	17	0.6	203	5	US-09-237-183A-115 Sequence 115, App
24	17	0.6	203	5	US-09-371-146A-54399 Sequence 54399, A
25	17	0.6	204	5	US-09-237-183A-108 Sequence 108, App
26	17	0.6	204	5	US-09-371-146A-2129 Sequence 2129, App
27	17	0.6	209	5	US-09-237-183A-117 Sequence 117, App

C 28	17	0.6	212	5	US-09-237-183A-130	Sequence 130, App
C 29	17	0.6	212	5	US-09-371-146A-42667	Sequence 42667, A
C 30	17	0.6	216	5	US-09-237-183A-106	Sequence 106, App
C 31	17	0.6	216	5	US-09-237-183A-118	Sequence 118, App
C 32	17	0.6	216	5	US-09-371-146A-55273	Sequence 55273, A
C 33	17	0.6	216	5	US-09-371-146A-62741	Sequence 62741, A
C 34	17	0.6	216	5	US-09-237-183A-121	Sequence 121, App
C 35	17	0.6	238	5	US-09-371-146A-18923	Sequence 18923, A
C 36	17	0.6	240	5	US-09-237-183A-129	Sequence 129, App
C 37	17	0.6	240	5	US-09-371-146A-19740	Sequence 19740, A
C 38	17	0.6	243	5	US-09-371-146A-70051	Sequence 70051, A
C 39	17	0.6	246	5	US-09-237-183A-128	Sequence 128, App
C 40	17	0.6	246	5	US-09-371-146A-22844	Sequence 22844, A
C 41	17	0.6	255	5	US-09-237-183A-116	Sequence 116, App
C 42	17	0.6	255	5	US-09-371-146A-4552	Sequence 4552, App
C 43	17	0.6	259	5	US-09-237-183A-112	Sequence 112, App
C 44	17	0.6	259	5	US-09-371-146A-22925	Sequence 22925, A
C 45	17	0.6	260	5	US-09-237-183A-156	Sequence 156, App

#### ALIGNMENTS

```

RESULT 1
US-09-560-875A-7981
; Sequence 7981, Application US/09560875A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Slinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 787
; CURRENT APPLICATION NUMBER: US/09/560,875A
; CURRENT FILING DATE: 2000-04-27
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10410
; SOFTWARE: PC_CT_genes Version 1.02
; SEQ ID NO 7981
; LENGTH: 3836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3836)
; OTHER INFORMATION: n = a,t,c or g
; NAME/KEY: misc_feature
; LOCATION: (28)...(3024)
; OTHER INFORMATION: similar to g1406868 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3f00, default parameters
US-09-560-875A-7981

Query Match 1.0%; Score 30; DB 5; Length 3836;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 GGGTGGAGAGGTGAGTGCCTACGATGAG 111
Db 208 ggggtgggaagaggtgagtgagctacgatgag 237

RESULT 2
US-09-872-850-298
; Sequence 298, Application US/09872850
; GENERAL INFORMATION:
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Escobedo, Jaime
; APPLICANT: Reinhard, Christoph
; APPLICANT: Randazzo, Filippo
; APPLICANT: Lamson, George

```

APPLICANT: Garcia, Pablo  
APPLICANT: Kaufmann, Joerg  
APPLICANT: Kennedy, Giulia  
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
TITLE OF INVENTION: IN CANCEROUS COLON CELLS  
FILE REFERENCE: 15805.002  
CURRENT APPLICATION NUMBER: US/09/872.850  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 60/208,871  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: fastseq for windows Version 4.0  
SEQ ID NO 298  
LENGTH: 399  
TYPE: DNA  
ORGANISM: sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(399)  
OTHER INFORMATION: n = A,T,C or G  
US-09-872-850-298

Query Match 0.8%; Score 23; DB 5; Length 399;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 GTCACAGCACTGCTGCTGCAA 2234  
|||||  
Db 54 gtcaacagcaacctgctgctgcaa 76

RESULT 3  
US-09-872-850-301  
Sequence 301, Application US/09872850  
GENERAL INFORMATION:  
APPLICANT: Sudduth-Klinger, Julie  
APPLICANT: Escobedo, Jaime  
APPLICANT: Reinhard, Christoph  
APPLICANT: Randazzo, Filippo  
APPLICANT: Lamson, George  
APPLICANT: Garcia, Pablo  
APPLICANT: Kaufmann, Joerg  
APPLICANT: Kennedy, Giulia  
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
TITLE OF INVENTION: IN CANCEROUS COLON CELLS  
FILE REFERENCE: 15805.002  
CURRENT APPLICATION NUMBER: US/09/872,850  
CURRENT FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: 60/208,871  
PRIOR FILING DATE: 2000-06-02  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: fastseq for windows Version 4.0  
SEQ ID NO 301  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(504)  
OTHER INFORMATION: n = A,T,C or G  
US-09-872-850-301

Query Match 0.8%; Score 23; DB 5; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 GTCACAGCACTGCTGCTGCAA 2234  
|||||  
Db 45 gtcaacagcaacctgctgctgcaa 67

RESULT 4  
US-09-771-161A-4  
Sequence 4, Application US/09771161A  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 2451  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: -  
LOCATION: (1)...(2451)  
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-4

Query Match 0.8%; Score 23; DB 5; Length 2451;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2326 TGGACAGCCCCGAGAGCCATCCA 2348  
|||||  
Db 1636 ttgacagccccgagagccatcca 1658

RESULT 5  
US-09-560-875A-6907  
Sequence 6907, Application US/09560875A  
GENERAL INFORMATION:  
APPLICANT: Tang, Yuanhua T.  
APPLICANT: Tillinghast, John  
APPLICANT: Sinku, Ankura  
APPLICANT: Liu, Chenshua  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: Novel Contigs Obtained  
TITLE OF INVENTION: From Various Libraries  
FILE REFERENCE: 787  
CURRENT APPLICATION NUMBER: US/09/560,875A  
CURRENT FILING DATE: 2000-04-27  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 10410  
SOFTWARE: PL\_CT\_genes Version 1.02  
SEQ ID NO 6907  
LENGTH: 4016  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (712)...(3830)  
OTHER INFORMATION: similar to g11177466 in the genepept database release 114,  
OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
US-09-560-875A-6907

Query Match 0.7%; Score 21; DB 5; Length 4016;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GAGTGCTGTGCTGCCATCGG 714  
|||||  
Db 1552 gagtgcgtgtgctgccatcggg 1572

## RESULT 6

US-09-693-692-967  
; Sequence 967, Application US/09693692  
; GENERAL INFORMATION:  
; APPLICANT: Nehls, Michael  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Human Polynucleotides and  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: LEX-0073-USA  
; CURRENT APPLICATION NUMBER: US/09/693,692  
; CURRENT FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: US 60/161,622  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 1665  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 967  
; LENGTH: 382  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(382)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-693-692-967

## Query Match

0.6%; Score 19; DB 5; Length 382;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1610 TCTTCCTCATGCTGCTGCTG 1628

DB 36 tcttcctcatgctgctgctg 54

## RESULT 7

PCT-US01-10485A-316  
; Sequence 316, Application PC/TUS0110485A  
; GENERAL INFORMATION:  
; APPLICANT: Genetics Institute, Inc.  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Graham, James R.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6402PC  
; CURRENT APPLICATION NUMBER: PCT/US01/10485A  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/195,604  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 631  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 316  
; LENGTH: 2083  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US01-10485A-316

## Query Match

0.6%; Score 19; DB 1; Length 2083;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 888 CAGAGCAGACTGACGCC 906

DB 1946 cagagcagactgacgcc 1964

## RESULT 8

US-09-560-875A-7710  
; Sequence 7710, Application US/09560875A  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Yuanhua T.  
; APPLICANT: Tillinghast, John  
; APPLICANT: Sinku, Ankura  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Contigs Obtained  
; TITLE OF INVENTION: From Various Libraries  
; FILE REFERENCE: 787  
; CURRENT APPLICATION NUMBER: US/09/560,875A  
; CURRENT FILING DATE: 2000-04-27  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10410  
; SOFTWARE: PLCT\_genes Version 1.02  
; SEQ ID NO 7710  
; LENGTH: 5374  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (174)...(3847)  
; OTHER INFORMATION: similar to g12695574 in the genepept database release 114,  
US-09-560-875A-7710

## Query Match

0.6%; Score 19; DB 5; Length 5374;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2182 CACGCTGACCTGCGTGC 2200

DB 1391 caccgtgacctgcgcgc 1409

## RESULT 9

US-09-793-706A-3/C  
; Sequence 3, Application US/09793706A  
; GENERAL INFORMATION:  
; APPLICANT: GONG, Fancheng et al  
; TITLE OF INVENTION: ISOLATED HUMAN TUMOR SUPPRESSOR PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN TUMOR SUPPRESSOR  
; FILE REFERENCE: C1001145  
; CURRENT APPLICATION NUMBER: US/09/793,706A  
; CURRENT FILING DATE: 2001-02-27  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 163350  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(163350)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-793-706A-3

## Query Match

0.6%; Score 19; DB 5; Length 163350;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 CCCACGCTGCTGCTGC 276

DB 123562 CCCACGCTGCTGCTGC 123544

RESULT 10  
US-08-221-623D-2326  
; Sequence 2326, Application US/08221623D  
; GENERAL INFORMATION:  
; APPLICANT: Adams, et al.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products  
; FILE REFERENCE: PO-10  
; CURRENT APPLICATION NUMBER: US/08/221,623D  
; CURRENT FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 3321  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2326  
; LENGTH: 207  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (63)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (140)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc\_feature  
; LOCATION: (175)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-08-221-623D-2326

Query Match 0.6%; Score 18; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1143 CAGTGACCTGCTGCCCA 1160  
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Db 1 cagtgacctgctgcccga 18

RESULT 11  
US-09-371-146A-12431/c  
; Sequence 12431, Application US/09371146A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: ANNOTATED PLANT GENES  
; FILE REFERENCE: 38-21(15097)C  
; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 12431  
; LENGTH: 327  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-371-146A-12431

Query Match 0.6%; Score 18; DB 5; Length 327;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 AGGAGACCTTCAACCTCT 298  
|||||

Db 59 AGGAGACCTTCAACCTCT 42

RESULT 12  
US-09-649-165A-760  
; Sequence 760, Application US/09649165A  
; GENERAL INFORMATION:  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Doyle, Martin  
; APPLICANT: Momiyama, Monika

APPLICANT: Wang, Xinhao  
; TITLE OF INVENTION: DETECTING EXPRESSION OF ARABIDOPSIS THALIANA GENES  
; FILE REFERENCE: PA-0019 US  
; CURRENT APPLICATION NUMBER: US/09/649,165A  
; CURRENT FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/150,517  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 7753  
; SOFTWARE: PERL Program  
; SEQ ID NO 760  
; LENGTH: 487  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: lacyte ID No: 701495952  
US-09-649-165A-760

Query Match 0.6%; Score 18; DB 5; Length 487;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGAACCTGTCGCGG 597  
|||||

Db 393 caggaacctgctcgcg 410

RESULT 13  
US-09-371-146A-253158/c  
; Sequence 253158, Application US/09371146A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: ANNOTATED PLANT GENES  
; FILE REFERENCE: 38-21(15097)C  
; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 253158  
; LENGTH: 525  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-371-146A-253158

Query Match 0.6%; Score 18; DB 5; Length 525;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1031 ACAACATCATCTGCAGA 1048  
|||||

Db 230 ACAACATCATCTGCAGA 213

RESULT 14  
US-09-237-183A-5/c  
; Sequence 5, Application US/09237183A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Liu, Jindong  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The  
; FILE REFERENCE: 38-21(15089)B  
; CURRENT APPLICATION NUMBER: US/09/237,183A  
; CURRENT FILING DATE: 1999-01-26  
; PRIOR APPLICATION NUMBER: US 60/067,000  
; PRIOR FILING DATE: 1997-11-24  
; NUMBER OF SEQ ID NOS: 2814  
; SEQ ID NO 5

LENGTH: 109  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-237-183A-5

Query Match 0.6%; Score 17; DB 5; Length 109;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 GGTCCGAGACTTCGAC 460  
|||||  
DB 74 GGTCCGAGACTTCGAC 58

RESULT 15  
US-09-237-183A-133/C  
Sequence 133, Application US/09237183A  
GENERAL INFORMATION:  
APPLICANT: Chelkh, Nordine  
APPLICANT: Fisher, Dane K.  
APPLICANT: Liu, Jingdong  
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The  
FILE REFERENCE: 38-21(15089)B  
CURRENT APPLICATION NUMBER: US/09/237,183A  
PRIOR APPLICATION NUMBER: US 60/067,000  
PRIOR FILING DATE: 1997-11-24  
NUMBER OF SEQ ID NOS: 2814  
SEQ ID NO 133  
LENGTH: 128  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-237-183A-133

Query Match 0.6%; Score 17; DB 5; Length 128;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 GGTCCGAGACTTCGAC 460  
|||||  
DB 55 GGTCCGAGACTTCGAC 39

Search completed: July 10, 2001, 22:21:38  
Job time: 7775 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 15:07:58 ; Search time 3870.77 Seconds

(without alignments)  
11836.269 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CTGCTGCCCGCCGTGAGAGA.....CCAGCCCCCGCCCTCTGC 2962

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBdb1: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_ba3: \*  
4: gb\_in1: \*  
5: gb\_in2: \*  
6: gb\_in3: \*  
7: gb\_om: \*  
8: gb\_ov: \*  
9: gb\_pat1: \*  
10: gb\_pat2: \*  
11: gb\_ph: \*  
12: gb\_pl1: \*  
13: gb\_pl2: \*  
14: gb\_pl3: \*  
15: gb\_pl4: \*  
16: em\_ba1: \*  
17: em\_ba2: \*  
18: em\_fun: \*  
19: em\_htgo\_hum: \*  
20: em\_htgo\_inv: \*  
21: em\_htgo\_rtd: \*  
22: em\_htg\_hum1: \*  
23: em\_htg\_hum2: \*  
24: em\_htg\_hum3: \*  
25: em\_htg\_hum4: \*  
26: em\_htg\_hum5: \*  
27: em\_htg\_hum6: \*  
28: em\_htg\_hum7: \*  
29: em\_htg\_hum8: \*  
30: em\_htg\_inv1: \*  
31: em\_htg\_inv2: \*  
32: em\_htg\_other: \*  
33: em\_htg\_rtd: \*  
34: em\_hum1: \*  
35: em\_hum2: \*  
36: em\_hum3: \*  
37: em\_hum4: \*  
38: em\_hum5: \*  
39: em\_hum6: \*  
40: em\_hum7: \*  
41: em\_in: \*  
42: em\_om: \*  
43: em\_or: \*

44: em\_ov: \*  
45: em\_pat: \*  
46: em\_ph: \*  
47: em\_pl: \*  
48: em\_ro: \*  
49: em\_sts: \*  
50: em\_sy: \*  
51: em\_un: \*  
52: em\_v1: \*  
53: gb\_sts1: \*  
54: gb\_sts2: \*  
55: gb\_sts3: \*  
56: gb\_sy: \*  
57: gb\_un: \*  
58: gb\_v11: \*  
59: gb\_v12: \*  
60: gb\_v13: \*  
61: gb\_v14: \*  
62: gb\_v15: \*  
63: gb\_v16: \*  
64: gb\_v17: \*  
65: gb\_v18: \*  
66: gb\_v19: \*  
67: gb\_v20: \*  
68: gb\_v21: \*  
69: gb\_v22: \*  
70: gb\_v23: \*  
71: gb\_v24: \*  
72: gb\_v25: \*  
73: gb\_v26: \*  
74: gb\_v27: \*  
75: gb\_v28: \*  
76: gb\_v29: \*  
77: gb\_v30: \*  
78: gb\_v31: \*  
79: gb\_v32: \*  
80: gb\_v33: \*  
81: gb\_v34: \*  
82: gb\_v35: \*  
83: gb\_v36: \*  
84: gb\_v37: \*  
85: gb\_v38: \*  
86: gb\_v39: \*  
87: gb\_v40: \*  
88: gb\_v41: \*  
89: gb\_v42: \*  
90: gb\_v43: \*  
91: gb\_v44: \*  
92: gb\_v45: \*  
93: gb\_v46: \*  
94: gb\_v47: \*  
95: gb\_v48: \*  
96: gb\_v49: \*  
97: gb\_v50: \*  
98: em\_ba3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2962	100.0	2962	9 AR084933	AR084933 Sequence
2	2962	100.0	2962	9 AR084949	AR084949 Sequence
3	2961.6	100.0	2962	97 HUMRPTKA	L36643 Homo sapien
4	2923.4	98.7	3768	9 AX034853	AX034853 Sequence
5	2923.4	98.7	3768	97 HUMDRRT	L41939 Homo sapien
6	2897.2	97.8	3151	97 HUMERRA	D31661 Human mRNA
7	2884	97.4	3949	9 AX034855	AX034855 Sequence
8	2884	97.4	3949	88 AF025304	AF025304 Homo sapi

9	2498	84.3	3104	94	MUSNRK	L25890 Mus musculi
10	2185.6	73.8	3227	8	CHCKE5	M62325 Chicken emb
11	2185.6	72.7	4049	11	I15008	I15008 Sequence 17
12	2153.8	72.7	3060	8	CCOEK5PRT	X91737 C.colurnix
13	2127.6	71.8	4097	10	I15005	I15005 Sequence 11
14	1652	55.8	2664	8	AF026039	AF026039 Xenopus 1
15	1642.2	55.4	3871	97	H0MEPRT2R	L40636 Homo sapien
16	1634.2	55.2	4400	95	RATELKE	M59814 Rattus norv
17	1632.6	55.1	3823	88	AF037331	AF037331 Homo sapi
18	1609.6	54.3	7261	93	AF037332	AF037332 Homo sapi
19	1588.2	53.6	3805	93	H5PTRK	X75208 H.sapiens H
20	1581.6	53.4	3546	10	I15004	I15004 Sequence 9
21	1543.4	52.1	3591	8	GCCEK10A	Z19061 G.gallus Ce
22	1543.4	52.1	3591	10	I15006	I15006 Sequence 13
23	1526.4	51.5	4027	9	A44406	A44406 Sequence 3
24	1526.4	51.5	4027	9	A44407	A44407 Sequence 4
25	1526.4	51.5	4027	9	AR038072	AR038072 Sequence
26	1526.4	51.5	4027	9	AR038073	AR038073 Sequence
27	1526.4	51.5	4027	10	I19547	I19547 Sequence 3
28	1526.4	51.5	4027	10	I19548	I19548 Sequence 4
29	1526.4	51.5	4027	45	E09831	E09831 cDNA encodi
30	1520.8	51.3	2982	9	A44405	A44405 Sequence 2
31	1520.8	51.3	2982	9	AR038071	AR038071 Sequence
32	1520.8	51.3	2982	10	I19546	I19546 Sequence 2
33	1504.2	50.8	4010	94	MMMDK5	Z49086 M.musculus
34	1471.6	49.7	3135	8	GCCEK6A	Z19110 G.gallus Ce
35	1470	49.6	1618	97	HUMERK1P	D37827 Homo sapien
36	1469.6	49.6	3133	10	I15000	I15000 Sequence 1
37	1456.8	49.2	4455	8	XL014164	U11493 Mus musculu
38	1426.6	48.2	3584	94	MMU01493	U11493 Mus musculu
39	1410.2	47.6	2839	88	AF037333	AF037333 Homo sapi
40	1398.2	47.2	3346	8	XELERTKA	L43621 Xenopus lae
41	1240.2	41.9	1635	94	MMSEK3	X76011 M.musculus
42	1204	40.6	4244	8	XELERTK	L43620 Xenopus lae
43	1201.2	40.4	3712	8	GGU23783	U23783 Gallus gall
44	1196.8	40.4	3776	10	I15003	I15003 Sequence 7
45	1079	36.4	3544	94	BC004782	BC004782 Mus muscu

ALIGNMENTS

RESULT 1	AR084933	2962 bp	DNA	PAT	01-SEP-2000
LOCUS	AR084933	Sequence 10	from patent US 5981245.		
DEFINITION	AR084933				
ACCESSION	AR084933				
VERSION	AR084933.1	GI:10011704			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2962)				
AUTHORS	Fox,G.M., Welcher,A.A. and Jing,S.				
TITLE	EPH-A-like receptor protein tyrosine kinases				
JOURNAL	Patent: US 5981245-A 10 09-NOV-1999;				
FEATURES	Location/Qualifiers				
source	1.2962				
BASE COUNT	654 a 914 c 827 g 567 t				
ORIGIN	/organism="unknown"				

Query Match 100.0%; Score 2962; DB 9; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTGCTGCGCCGCTGGAGAAACGTAATGACTCCACTACAGAGAGCTGTGAGTGGGC	60
DB	1	CTGCTGCGCCGCTGGAGAAACGTAATGACTCCACTACAGAGAGCTGTGAGTGGGC	60
QY	61	TGGATGATGATCCTCATCAGAGGTTGGGAGAGAGTGTGCTACGATGAGAAACATGAAC	120
DB	1	TGGATGATGATCCTCATCAGAGGTTGGGAGAGAGTGTGCTACGATGAGAAACATGAAC	120

DB	61	TGGATGATGATCCTCATCAGAGGTTGGGAGAGAGTGTGCTACGATGAGAAACATGAAC	120
QY	121	ACGATCGGACACGATACAGAGTGTGCAACGTTTGTGATGCAAGCAACACTGGCTACGG	180
DB	121	ACGATCGGACACGATACAGAGTGTGCAACGTTTGTGATGCAAGCAACACTGGCTACGG	180
QY	181	ACCAAGTTTATTCGAGGCGCGTGGGCGCCACCCGATCCAGCTGAGATGTAAGTTTGGTG	240
DB	181	ACCAAGTTTATTCGAGGCGCGTGGGCGCCACCCGATCCAGCTGAGATGTAAGTTTGGTG	240
QY	241	CGTACTGACGACGACATCCCGACGCTGCTGCTGCTGCAAGAGACCTTCAACTCTAT	300
DB	241	CGTACTGACGACGACATCCCGACGCTGCTGCTGCTGCTGCAAGAGACCTTCAACTCTAT	300
QY	301	TACTATGAGGCTACCTTGTGCTGGCCACCAACCTTCCCAAGTGAAGTGAATCA	360
DB	301	TACTATGAGGCTACCTTGTGCTGGCCACCAACCTTCCCAAGTGAAGTGAATCA	360
QY	361	TGGGTGAGGTGAGATACCATTTGACGCGACGAGAGCTTCCAGGTTGACCTGGGTGGC	420
DB	361	TGGGTGAGGTGAGATACCATTTGACGCGACGAGAGCTTCCAGGTTGACCTGGGTGGC	420
QY	421	CGCGTATGAAATCAACACCGAGGTGCGAGCTTGTGCTGCTGCTGCTGCTGCTTAC	480
DB	421	CGCGTATGAAATCAACACCGAGGTGCGAGCTTGTGCTGCTGCTGCTGCTGCTTAC	480
QY	481	TACTGCGCTTCGAGACTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAC	540
DB	481	TACTGCGCTTCGAGACTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAC	540
QY	541	CGCAAGTGGCCCGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT	600
DB	541	CGCAAGTGGCCCGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT	600
QY	601	GAGAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
DB	601	GAGAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
QY	661	GTAACCATCATGAGCTTACTGTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720
DB	661	GTAACCATCATGAGCTTACTGTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720
QY	721	ATGTGCAAAAGCAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
DB	721	ATGTGCAAAAGCAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
QY	781	GGAATTTTCAAGGCGCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840
DB	781	GGAATTTTCAAGGCGCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840
QY	841	ACCACTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	900
DB	841	ACCACTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	900
QY	901	GACCCCTGAGATGCGCTGACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	960
DB	901	GACCCCTGAGATGCGCTGACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	960
QY	961	GTCATATGAGACCTTCCCTCATGCTGAGTGAACCCCTCCCGGCACTCCGAGGAGG	1020
DB	961	GTCATATGAGACCTTCCCTCATGCTGAGTGAACCCCTCCCGGCACTCCGAGGAGG	1020
QY	1021	GACCTGCTACAAATCATCTGCAAGAGTGTGGTGGGAGGAGGAGGAGGAGGAGGAGG	1080
DB	1021	GACCTGCTACAAATCATCTGCAAGAGTGTGGTGGGAGGAGGAGGAGGAGGAGGAGG	1080
QY	1081	TGGGAGGAGACATATACAGTACGACCAACGAGCTGAGGCTGACGAGCAGCAATTTAC	1140
DB	1081	TGGGAGGAGACATATACAGTACGACCAACGAGCTGAGGCTGACGAGCAGCAATTTAC	1140
QY	1141	ATCAGTACCTGCTGCGCCACACCCAGTACACCTTGAAGTTCAGGCTGTGAAGCGCG	1200
DB	1141	ATCAGTACCTGCTGCGCCACACCCAGTACACCTTGAAGTTCAGGCTGTGAAGCGCG	1200



QY 1201 ACTGACAGAGCCCTTCTGCGCTCACTTGCCCTCTGTGAACATCACCACCAAGGCA 1250  
 |||||||  
 Db 1201 ACTGACAGAGCCCTTCTGCGCTCACTTGCCCTCTGTGAACATCACCACCAAGGCA 1250  
 QY 1261 GCTTCATCGGAGTGTCTATCATCATCAGTGTGAGCGGCGGCGGAGAGATTAACCTG 1320  
 |||||||  
 Db 1261 GCTTCATCGGAGTGTCTATCATCATCAGTGTGAGCGGCGGCGGAGAGATTAACCTG 1320  
 QY 1321 TCGGTGTCCAGCGGAGCAAGCCCAATGGCGTGTGATCTGACATATGAGCTCACTACTAT 1380  
 |||||||  
 Db 1321 TCGGTGTCCAGCGGAGCAAGCCCAATGGCGTGTGATCTGACATATGAGCTCACTACTAT 1380  
 QY 1381 GAGAGAGAGCTCACTGAGTACACGCAACAGCCATAAAAAGCCCAACACAGGTCACG 1440  
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 Db 1381 GAGAGAGAGCTCACTGAGTACACGCAACAGCCATAAAAAGCCCAACACAGGTCACG 1440  
 QY 1441 GGCTCAAGAGCGGCGGCGCTATGTCTTCCAGTGGGCGGAGCAGCTGTGGCAGGCTAC 1500  
 |||||||  
 Db 1441 GGCTCAAGAGCGGCGGCGCTATGTCTTCCAGTGGGCGGAGCAGCTGTGGCAGGCTAC 1500  
 QY 1501 GGGGCTACAGCGGCAAGATTAATCTCCAGACATGACAGAGCGGAGTACAGACAGC 1560  
 |||||||  
 Db 1501 GGGGCTACAGCGGCAAGATTAATCTCCAGACATGACAGAGCGGAGTACAGACAGC 1560  
 QY 1561 ATCCAGAGAGAGTGTGCGCATCATCGGCTCTGCGGCGGCTGGCTGTGCTCTCAT 1620  
 |||||||  
 Db 1561 ATCCAGAGAGAGTGTGCGCATCATCGGCTCTGCGGCGGCTGGCTGTGCTCTCAT 1620  
 QY 1621 GCTGTGTGTCTATCGGCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
 |||||||  
 Db 1621 GCTGTGTGTCTATCGGCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
 QY 1681 TACACGAGCAAGTGTCAACACTTACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
 |||||||  
 Db 1681 TACACGAGCAAGTGTCAACACTTACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740  
 QY 1741 ATCCAGAGAGAGTGTGCGCATCATCGGCTCTGCGGCGGCTGGCTGTGCTCTCAT 1800  
 |||||||  
 Db 1741 ATCCAGAGAGAGTGTGCGCATCATCGGCTCTGCGGCGGCTGGCTGTGCTCTCAT 1800  
 QY 1801 GACATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
 |||||||  
 Db 1801 GACATCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
 QY 1861 AGTGGCCACCTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920  
 |||||||  
 Db 1861 AGTGGCCACCTGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920  
 QY 1921 TCGGGCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
 |||||||  
 Db 1921 TCGGGCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
 QY 1981 TTGACACATCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
 |||||||  
 Db 1981 TTGACACATCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
 QY 2041 ATCATACACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100  
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 Db 2041 ATCATACACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100  
 QY 2101 CAGTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160  
 |||||||  
 Db 2101 CAGTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160  
 QY 2161 CTGGCAGACATGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220  
 |||||||  
 Db 2161 CTGGCAGACATGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220  
 QY 2221 AACCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280  
 |||||||  
 Db 2221 AACCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280

QY 2281 GACCCACCTACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340  
 |||||||  
 Db 2281 GACCCACCTACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340  
 QY 2341 GGCATCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400  
 |||||||  
 Db 2341 GGCATCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400  
 QY 2401 TGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460  
 |||||||  
 Db 2401 TGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460  
 QY 2461 AATGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520  
 |||||||  
 Db 2461 AATGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520  
 QY 2521 CAATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580  
 |||||||  
 Db 2521 CAATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580  
 QY 2581 GTCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640  
 |||||||  
 Db 2581 GTCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640  
 QY 2641 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700  
 |||||||  
 Db 2641 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700  
 QY 2701 ACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760  
 |||||||  
 Db 2701 ACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2760  
 QY 2761 GCGGCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820  
 |||||||  
 Db 2761 GCGGCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820  
 QY 2821 GGGGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880  
 |||||||  
 Db 2821 GGGGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2880  
 QY 2881 CAGATGAACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
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 Db 2881 CAGATGAACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
 QY 2941 CTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2962  
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 Db 2941 CTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2962  
 RESULT 2  
 AR084949 2962 bp DNA PAT 01-SEP-2000  
 LOCUS AR084949 Sequence 10 from patent US 5981246.  
 DEFINITION AR084949  
 ACCESSION AR084949.1 GI:10011720  
 VERSION AR084949.1  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2962)  
 AUTHORS Fox, G.M., Welcher, A.A. and Jing, S.  
 TITLE Nucleic acids encoding Eph-like receptor protein tyrosine kinases  
 JOURNAL Patent: US 5981246-A 10 09-NOV-1999;  
 FEATURES Location/Qualifiers  
 source 1..2962  
 BASE COUNT 654 a 914 c 827 g 567 t  
 ORIGIN  
 Query Match 100.0%; Score 2962; DB 9; Length 2962;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGTCGCGCCGCGTGAAGAAAGCTATGAGCTCCACTACAGGACTGCTGAGCTGGGC 60  
Db 1 CTGTCGCGCCGCGTGAAGAAAGCTATGAGCTCCACTACAGGACTGCTGAGCTGGGC 60  
QY 61 TGGATGCTGATCTCCATCAGAGGTGGGAAGAGGTGAGTGGCTACATGAGACATGAAC 120  
Db 61 TGGATGCTGATCTCCATCAGAGGTGGGAAGAGGTGAGTGGCTACATGAGACATGAAC 120  
QY 121 ACCATCCGACGATACCAAGGTGTGCAACGCTTTGATGCAAGCCAGAACAACCTGGCTACGG 180  
Db 121 ACCATCCGACGATACCAAGGTGTGCAACGCTTTGATGCAAGCCAGAACAACCTGGCTACGG 180  
QY 181 ACCAAGTTATCCGGGCGCGTGGGGGCCACCGCATCCACGTTGAGATGAAGTTTGGTG 240  
Db 181 ACCAAGTTATCCGGGCGCGTGGGGGCCACCGCATCCACGTTGAGATGAAGTTTGGTG 240  
QY 241 CGTACTGACAGACATCCCGAGCGTCTGGCTCTGCAAGAGACCTTCAACCTCTAT 300  
Db 241 CGTACTGACAGACATCCCGAGCGTCTGGCTCTGCAAGAGACCTTCAACCTCTAT 300  
QY 301 TACTATGAGGCTACTTTGATCTGGGCGCCACCAAGACCTTCCCAACTGGATGAGATCCA 360  
Db 301 TACTATGAGGCTACTTTGATCTGGGCGCCACCAAGACCTTCCCAACTGGATGAGATCCA 360  
QY 361 TGGGTGAAGGTGATACCATTTGACGCGGACGAGAGCTTCCAGGTGAGCTGGGTGGC 420  
Db 361 TGGGTGAAGGTGATACCATTTGACGCGGACGAGAGCTTCCAGGTGAGCTGGGTGGC 420  
QY 421 CGGCTCATGAAATCAACACCGAGGTGCGAGCTTCCGACCTGTGTCCGACGCGCTTC 480  
Db 421 CGGCTCATGAAATCAACACCGAGGTGCGAGCTTCCGACCTGTGTCCGACGCGCTTC 480  
QY 481 TACTGCGCTCCAGAGCTATGGGCGCTGATGCTCCTCATCCGCGCTGCTTCTTAC 540  
Db 481 TACTGCGCTCCAGAGCTATGGGCGCTGATGCTCCTCATCCGCGCTGCTTCTTAC 540  
QY 541 CGCAAGTGCCTCCGATCATCCAGAAATGGCGCATCTTCCAGGAAACCTGTGGGGGCT 600  
Db 541 CGCAAGTGCCTCCGATCATCCAGAAATGGCGCATCTTCCAGGAAACCTGTGGGGGCT 600  
QY 601 GAGAGCATGCTGCTGGTGGTCCCGGGGAGCTGATGCTGCGCAATGCGGAAGAGTGGAT 660  
Db 601 GAGAGCATGCTGCTGGTGGTCCCGGGGAGCTGATGCTGCGCAATGCGGAAGAGTGGAT 660  
QY 661 GTACCATCAAGCTACTGCTAAGGGGAGGAGGAGTGGTGGTGGCCATCGGGCGCTGC 720  
Db 661 GTACCATCAAGCTACTGCTAAGGGGAGGAGGAGTGGTGGTGGCCATCGGGCGCTGC 720  
QY 721 ATGTGCAAGCAGGCTTGAAGGCGCTTGAAGATGAGCACTGCTGCGGAGGTTTGTCACT 780  
Db 721 ATGTGCAAGCAGGCTTGAAGGCGCTTGAAGATGAGCACTGCTGCGGAGGTTTGTCACT 780  
QY 781 GGGACTTTTCAGGCCAACCAAGGGGATGAGGCTGTACCCCATGCTCCCATCAACAGCGG 840  
Db 781 GGGACTTTTCAGGCCAACCAAGGGGATGAGGCTGTACCCCATGCTCCCATCAACAGCGG 840  
QY 841 ACCACTTTCGAAGGGGCGAACCACTGCTGCGCAATGGCTACTACAGAGACACTG 900  
Db 841 ACCACTTTCGAAGGGGCGAACCACTGCTGCGCAATGGCTACTACAGAGACACTG 900  
QY 901 GACCCCTGACATGCTTGAAGGCGCAACCACTCCCGGCGCCAGGCTGTGATTTCCAGT 960  
Db 901 GACCCCTGACATGCTTGAAGGCGCAACCACTCCCGGCGCCAGGCTGTGATTTCCAGT 960  
QY 961 GTCAATGAGACCTGCTCATGCTGAGTGAAGCCCTCCCGGCGACTCCGAGGCGGAG 1020  
Db 961 GTCAATGAGACCTGCTCATGCTGAGTGAAGCCCTCCCGGCGACTCCGAGGCGGAG 1020  
QY 1021 GACCTGCTACAAATCATCTGCAAGAGCTGTGGGCGGGGGTGGCTGACACCGG 1080  
Db 1021 GACCTGCTACAAATCATCTGCAAGAGCTGTGGGCGGGGGTGGCTGACACCGG 1080

QY 1081 TGGGGGACATGTACAGTACGACCAAGCCAGCTAGGCTGAGCCGAGCCGACATTTAC 1140  
Db 1081 TGGGGGACATGTACAGTACGACCAAGCCAGCTAGGCTGAGCCGAGCCGACATTTAC 1140  
QY 1141 ATCAGTACCTGCTGAGCCACACCAAGTACACCTTGCAGATCCAGGCTGTGAAGGCGTT 1200  
Db 1141 ATCAGTACCTGCTGAGCCACACCAAGTACACCTTGCAGATCCAGGCTGTGAAGGCGTT 1200  
QY 1201 ACTGACCAAGGCGCTTCTGCGCTCAGTTGCGCTCTGTGAACATCACCAACCAAGGCA 1260  
Db 1201 ACTGACCAAGGCGCTTCTGCGCTCAGTTGCGCTCTGTGAACATCACCAACCAAGGCA 1260  
QY 1261 GCTTCATCGGACGATGCTCATCATGATCAGGTGAGCGGACCGCTGACATTTACCTG 1320  
Db 1261 GCTTCATCGGACGATGCTCATCATGATCAGGTGAGCGGACCGCTGACATTTACCTG 1320  
QY 1321 TCGTGTCCAGCGGACGACCCCAATGGCGTATCCTGAGATGAGCTGACGATAT 1380  
Db 1321 TCGTGTCCAGCGGACGACCCCAATGGCGTATCCTGAGATGAGCTGACGATAT 1380  
QY 1381 GAGAAGAGCTCAGTGAATCAACGCGCACAGCCATATAAAAGCCCCCAACAGGTCAG 1440  
Db 1381 GAGAAGAGCTCAGTGAATCAACGCGCACAGCCATATAAAAGCCCCCAACAGGTCAG 1440  
QY 1441 GGCCTCAAGCGCGGACATCTATGCTTCCAGGTGCGGACGACATGCGGAGGCTAC 1500  
Db 1441 GGCCTCAAGCGCGGACATCTATGCTTCCAGGTGCGGACGACATGCGGAGGCTAC 1500  
QY 1501 GGGCGCTACAGCGGCAAGATGTACTTCAGACCATGACAGACCGAGTACAGACAAAG 1560  
Db 1501 GGGCGCTACAGCGGCAAGATGTACTTCAGACCATGACAGACCGAGTACAGACAAAG 1560  
QY 1561 ATCCAGAGAGTTGTCACATCATCGCTCTCGGCGCTGGCTGGCTTCTCAT 1620  
Db 1561 ATCCAGAGAGTTGTCACATCATCGCTCTCGGCGCTGGCTGGCTTCTCAT 1620  
QY 1621 GCTGTGTTGTCATGCGCATCGTGTATACAGAGGGGATTTAGGCTGTGACTGGAG 1680  
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Qy	2221	AACCTGGTCTGCMAAGGTGTGGACATTGTGGGGCTTCACGCTTTCTAGAGACGATACCTCA	2280
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Qy	2341	GCCATCCATACCCGGAATTCACCTCCGCGACATGATGTGTGGAGCTACGGCATTTGTCATG	2400
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Qy	2461	AATGCCATTGACACAGACTATCGGCTGACACGGCCCATGTGACTGCCGACGCTTCGAC	2520
Db	2461	AATGCCATTGACACAGACTATCGGCTGACACGGCCCATGTGACTGCCGACGCTTCGAC	2520
Qy	2521	CAACATCATGCTGGATGTGTGGCAAGAAAGACCCGCAACCAACCGGCCCAAGTTGCGCAATT	2580
Db	2521	CAACATCATGCTGGATGTGTGGCAAGAAAGACCCGCAACCAACCGGCCCAAGTTGCGCAATT	2580
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Qy	2641	TGCTGTGGCATACACTGTCGCCCTGCTGTGACCGCGACAGATCCCGCATACCAAGCTTTAAC	2700
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RESULT	3		
HUMRPTKA			
LOCUS			
DEFINITION	Homo sapiens	2962 bp	10-AUG-1995
ACCESSION	L36643		
VERSION	L36643.1	GI:551609	
KEYWORDS	EPH-like receptor PTK; receptor protein-tyrosine kinase.		
SOURCE	Homo sapiens (clone library: Stratagene premade library, cat #36206)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	1 (bases 1 to 2962)		
	Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M.,		
	Basu,R. and Weischer,A.A.		
TITLE	cDNA cloning and tissue distribution of five human EPH-like		
	receptor protein-tyrosine kinases		

[illegible]

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LOCUS	AX034853			
DEFINITION	AX034853	3768 bp	DNA	PAT
ACCESSION	AX034853	Sequence 1	from Patent WO0053216.	15-NOV-2000
VERSION	AX034853.1	GI:11190805		
KEYWORDS				
SOURCE				
ORGANISM	human.			
REFERENCE	Human sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 (bases 1 to 3768)			
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BASE COUNT				
ORIGIN				

Query Match	98.7%	Score 2923.4	DB 9	Length 3768	
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Matches 2956	Conservative	0	Mismatches 6	Indels 9	Gaps 2
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Db	147	CTGCTCGCCGCGCGGTGGAGAAACGCTAATGAGCTCCACTACGCGACTGCTGAGTGGGC	206		
OY	61	TGAGTGGTGCATCTCCATCATCAGGTGGGGAAGAGTGGAGTGGCTTACGATGAGAACTGAAC	120		
Db	207	TGAGTGGTGCATCTCCATCATCAGGTGGGGAAGAGTGGAGTGGCTTACGATGAGAACTGAAC	266		
OY	121	ACGATCCGCACGTCACCAAGTGTGCAACGCTGTTTGAGTCAAGCCAGAACAACTGGCTACGG	180		
Db	267	ACGATCCGCACGTCACCAAGTGTGCAACGCTGTTTGAGTCAAGCCAGAACAACTGGCTACGG	326		
OY	181	ACCAAGTTTATCCGGGCGCGGTGGGGCCCAACGCGATCCACGTTGAGATGAAGTTTTCGGTG	240		
Db	327	ACCAAGTTTATCCGGGCGCGGTGGGGCCCAACGCGATCCACGTTGAGATGAAGTTTTCGGTG	386		
OY	241	CGTACATGCAACAGACTCCCAAGCGTGCCTGCTCTGCAAGAGAACCTTCAACTCTAT	300		

D	b	387	CGTGA	CTCAG	CAGAGAT	CCCA	GGGTG	CTGTG	CTGCA	AGAGAC	CTTCA	AACTCT	TA	446	
Q	y	301	TACTA	TGAG	GCTG	ACTTT	GACTG	GGCC	ACCA	AGACTT	TC	CCCA	TGAGTA	TA	360
D	b	447	TACTA	TGAG	GCTG	ACTTT	GACTG	GGCC	ACCA	AGACTT	TC	CCCA	TGAGTA	TA	506
Q	y	361	TGGG	GAAG	GTGG	TACCA	TGCA	GGCC	AGAG	AGCTT	CC	CAAG	TGGAG	CTG	420
D	b	507	TGGG	GAAG	GTGG	TACCA	TGCA	GGCC	AGAG	AGCTT	CC	CAAG	TGGAG	CTG	566
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D	b	567	CGC	GTCAT	GA	AAAT	CAAC	ACCG	AGGTG	CGAG	AGCTT	CG	AGAC	CGGCTT	626
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D	b	987	ACCA	CTT	TC	GA	AGG	GGC	ACCA	AGG	GGAT	GAG	GGC	CTT	1046
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D	b	1287	ATC	AG	TG	AC	CT	G	TG	CC	CA	AG	CA	CT	1348
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D	b	1407	GCT	CA	T	CG	CA	T	GG	CA	T	GG	CA	T	1466
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RESULT 5  
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 ACCESSION  
 141939.1 GI:1100109  
 VERSION  
 DRT gene: EPH gene family; protein-tyrosine kinase.  
 KEYWORDS  
 Homo sapiens (clone: FBK III 11c) (clone library: Stratagene,  
 Zapil, 936026) midterm fetus brain cDNA to mRNA.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 3768)  
 AUTHORS  
 Ikegaki,N., Tang,X.X., Liu,X.G., Biegel,J.A., Allen,C.,  
 Yoshioka,A., Sulman,E.P., Brodeur,G.M. and Pleasure,D.E.  
 TITLE  
 Molecular characterization and chromosomal localization of DRT  
 (EPH3): a developmentally regulated human protein-tyrosine kinase  
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 JOURNAL  
 Hum. Mol. Genet. 4 (11), 2033-2045 (1995)  
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DEFINITION	Human mRNA for tyrosine kinase, complete cds.
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VERSION	D31661.1 GI:495677
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REFERENCE	1 (sites)
AUTHORS	Iwase,T., Tanaka,M., Suzuki,M., Naito,Y., Sugimura,H. and Kino,I.
TITLE	Identification of protein-tyrosine kinase genes preferentially expressed in embryo stomach and gastric cancer
JOURNAL	Biochem. Biophys. Res. Commun. 194 (2), 698-705 (1993)
MEDLINE	933433925
REFERENCE	2 (bases 1 to 3151)
AUTHORS	Kiyokawa,E., Takai,S., Tanaka,M., Iwase,T., Suzuki,M., Xiang,Y.Y., Naito,Y., Yamada,K., Sugimura,H. and Kino,I.
TITLE	Overexpression of ERK, an EPH family receptor protein tyrosine kinase, in various human tumors
JOURNAL	Cancer Res. 54 (14), 3645-3650 (1994)
MEDLINE	94306360
REFERENCE	3 (bases 1 to 3151)
AUTHORS	Kiyokawa,E.
TITLE	Direct Submission
JOURNAL	Submitted (23-MAY-1994) to the DDBJ/EMBL/genbank databases. Etsuko Kiyokawa, Hamamatsu University School of Medicine, First Department of Pathology, 3600 Handa cho, Hamamatsu, Shizuoka 431-31, Japan (Tel:81-53-435-2220, Fax:81-53-435-2225)
COMMENT	Submitted (23-May-1994) to DDBJ by: Etsuko Kiyokawa Hamamatsu University School of Medicine First Department of Pathology 3600 Handa-cho Hamamatsu, Shizuoka 431-31 Japan Phone: 053-435-2220 Fax: 053-435-2225.
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## RESULT 7

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 3949)  
 AUTHORS Vinals, Y.D.  
 TITLE Novel uses  
 JOURNAL Patent: WO 0053216-A 3 14-SEP-2000;  
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VERSION	AF025304.1	GI:2739055	
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SOURCE	human.		
ORGANISM	Homo sapiens		
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AUTHORS	1 (bases 1 to 3949)		
TITLE	Ikegaki,N., Tang,X.X., Liu,X.G., Biegel,J.A., Allen,C., Yoshioka,A., Sulman,E.P., Brodeur,G.M., and Pleasure,D.E. Molecular characterization and chromosomal localization of DRT (EPHB2): a developmentally regulated human protein-tyrosine kinase gene of the Eph family		
JOURNAL	Hum. Mol. Genet.	4 (11),	2033-2045 (1995)
MEDLINE	96154673		
REFERENCE	2 (bases 1 to 3949)		
AUTHORS	Tang,X.X., Pleasure,D.E., Brodeur,G.M., and Ikegaki,N.		
TITLE	A variant transcript encoding an isoform of the human protein tyrosine kinase EPHB2 is generated by alternative splicing and alternative use of polyadenylation signals		
JOURNAL	Oncogene	17 (4),	521-526 (1998)
MEDLINE	98359217		
REFERENCE	3 (bases 1 to 3949)		
AUTHORS	Ikegaki,N. and Tang,X.X.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-SEP-1997)		
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MUSNRK 3104 bp mRNA ROD 05-NOV-1993

LOCUS Mus musculus Nuk receptor tyrosine kinase mRNA, complete cds.

DEFINITION L25890.1 GI:414593

VERSION L25890.1 GI:414593

KEYWORDS Nuk receptor tyrosine kinase.

SOURCE Mus musculus Embryo cDNA to mRNA.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3104)

AUTHORS Henkemeyer M.

TITLE Immunolocalization of the Nuk receptor tyrosine kinase suggests a role in segmental patterning of the brain and axonogenesis

JOURNAL Oncogene (1994) In press

FEATURES

source location/Qualifiers

1..3104

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FEATURES	LOCATION/Qualifiers	ORGANISM	VERSION	DATE
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LOCUS		Chicken embryo kinase 5 protein (CEK 5) mRNA, complete cds.		
DEFINITION		Chicken embryo kinase 5 protein (CEK 5) mRNA, complete cds.		
ACCESSION		M62325		
VERSION		M62325.1		
KEYWORDS		GI:211448		
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ORGANISM		Gallus gallus		
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REFERENCE		1 (bases 1 to 3227)		
AUTHORS		Pasquale,E.B.		
TITLE		Identification of chicken embryo kinase 5, a developmentally regulated receptor-type tyrosine kinase of the Eph family		
JOURNAL		Cell Regul. 2, 523-534 (1991)		
MEDLINE		92144672		
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Qy	2032	CCTGTGATGATCATCACCGAGATTCTATGGAATAGGGTCCCTGAGCATCCCTTCTCCGGCA	2091
Db	2116	CCAGTCATGATCATTTACAGAGATTCATGAGAAATGCTCTTGGATCTCTTCTTGAGGACA	2175
Qy	2092	AACGATGGCGATTTACAGTATCCAGCTGTGGAGGTGTGGATCTTTGGGGCATCGACGTGGC	2151
Db	2176	AATGATGGCGATTTCAAGATGATCCAGCTGTGGCATGTTCGATGGCATTTGACAGAGGC	2235
Qy	2152	ATGAAGTACCGGGAGACATGAATATGTTTCAACCCGTGACCTGGCTGCCCGCAACATCCTC	2211
Db	2236	ATGAAGTACCTGGCTGATATGAATCTGTGTACACGGGACCTGTGGCCCGCAACATCCTG	2295
Qy	2212	GTCAACAGCAACCTGTGTCAAGGTGTGTGGACTTGTGGCTGTCAAGCTTTCTAGAGAC	2271
Db	2296	GTCAACAGCAACCTGTGTCAAGGTGTGTGGACTTGTGGCTGTCAAGCTTTCTAGAGAT	2355
Qy	2272	GATTACTAGAGCCCACTTACCAAGTGGCCCTGTGGCGAAATTTCCCATCCGTGGACA	2331
Db	2356	GACACTCTGTATCCCACTTACACACAGCACTGTGGTGAAGATCCCAATCCGTTGGACA	2415
Qy	2332	GCCCCGGAAGCATTCAGTACCGGAATTTCACTCGGGCAGATGTGTGAGCTACGGC	2391
Db	2416	GCGGCTGAGCAATTCAGTACCGAAATTCACATCAGCGACAGAGATGTGTGAGCTATGGA	2475
Qy	2392	ATTGCAATGTGGAGAGTATGTCTTATGGGAGCGGCCCTACTGGAGCATGACCAACACG	2451
Db	2476	ATAGTCAATGTGGAGAGTATGTCTTATGGGAGCGGCCCTTACTGGAGCATGACCAATCA	2535
Qy	2452	GATGTAATCATGCAATTGAGCAGCACTTACGGCTGCGCACCGCCATGAGATGCTCCGAGC	2511
Db	2536	GATGTAATCATGCAATTGAGCAGCACTTACGGCTGCGCACCGCCATGAGATGCTCCGAAT	2595
Qy	2512	GCCTGCAACCACTATGCTGTGACTGTGTGGCAAGAGCAGCAACCGGCCCAAGTTTC	2571
Db	2596	GCCTGCAACCACTATGCTGTGACTGTGTGGCAAGAGTGTGGCAAGAGTGTGGCAAGTTTC	2655
Qy	2572	GGCCAAATTTCTCAACAGCGTAGACAAGATGATCCGATCCCAACAGCTCAAAAGCATG	2631
Db	2656	GAGCAGATGTCTCAACACTTTAGCAAAATGATCCGAATTTCTTAATGTGTGAAGGCATG	2715
Qy	2632	GGCGCCCTCTCTCTGTGGCATCAACCTGCCGCTGTGACCGCAGCATCCCGCATACCC	2691
Db	2716	GCACCTCTCTCTCTGTGGCTTAACCTCCCTCTACTTGAACCCACAAATCCCAATTTATCC	2775
Qy	2692	AGCTTTAACAAGGTGTGACAGAGTGGCTGGAGAGCCATCAAGATGGGGCAGTGTCAAGGAGAC	2751
Db	2776	AGCTTTAACAAGTGTGTGATATGCTGTGGATGCTCATCAAGATGAGCCAGTCAAGGAGAC	2835
Qy	2752	TTTGCCCAATGCGGGCTTCACTCTCTTTGACGTCTGTCTCGATGATGATGATGAGGAGCATT	2811
Db	2836	TTTGGCCAGTGTGCTGTTCACCACTTTGATATGATCTGAGATGATGATGAGGAGCATT	2895
Qy	2812	CTCCGGGTTGGGTCATTTGGCTGGCCACAGAAAAAATTCCTGAACAGTATTCACAGGTG	2871
Db	2896	CTACGAGTGTGGCTCACTTTACAGAGACACAGAAATTTCTGAACAGTATTCACAGGTG	2955

QY	2872	ATGGGGGGGAGATGAACAGATTCACATCTGTGTGAGGTTTGACATTTACCTGCTGGGCT	2931
Db	2956	ATGAGAGACAGATGAACAAATTCAGTCTGTGTGAGGTTTGATAGCAACAGTCTCTGTG	3015
QY	2932	CACCTCTTCCTCCACAGCCCGGCCCC	2957
Db	3016	CTCCATCTCTGTGAGGCTGTCTCC	3041
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LOCUS	115008	4049 bp	DNA
DEFINITION	Sequence 17 from patent US 5457048.		PAT
ACCESSION	115008		02-APR-1996
VERSION	115008.1	GI:1249916	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 4049)		
AUTHORS	Pasquale, E. B. and Sajjadi, F. G.		
TITLE	Eph-related tyrosine kinases, nucleotide sequences and methods of use		
JOURNAL	Patent: US 5457048-A 17 10-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..4049	/organism="unknown"	
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Query Match	73.8%;	Score 2185.6;	DB 10; Length 4049;
Best Local Similarity	84.1%;	Pred. No. 0;	
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QY	61	TGGATGTCATCTTCATCAGGTTGGGAAAGAGTGTGCTAGATGAGAATGTGAAC	120
Db	136	TGGATGTCATCTTCATCAGGTTGGGAAAGAGTGTGATGATGATGAGAATGTGAAC	195
QY	121	AGATCCGAGCTACACAGGTGTGCAACGCTTTGAGTCAAGCCAGAACACTGGCTACG	180
Db	196	ACCATCGACCTACACAGGTGTGCAACGCTTTGAGTCAAGCCAGAACACTGGCTACG	255
QY	181	ACCAAGTTATCCGGGCGCGTGGGCGCCACGSCATACAGGTGAGATGAAGTTCCGGG	240
Db	256	ACCAAGTTATCCGGGCGCGTGGGCGCCACGSCATACAGGTGAGATGAAGTTCCGGG	315
QY	241	CGTACGTGACGACGATCCCAAGCGTGGCTCTGTCAAGAGACCTTCAACCTCTAT	300
Db	316	CGGAGCTGACGACGATCCCAAGCGTGGCTCTGTCAAGAGACCTTCAACCTCTAT	375
QY	301	TACTATGAGGCGATGATTTGATCTGCGGCCACCAAGACCTTCCCACTGTGAGATCCA	360
Db	376	TACTATGATTCAGATCTTGTGACTCTGCCACCAAGACCTTCCCACTGTGAGATCCA	435
QY	361	TGGGTGAAGTGAATACCATTTGACAGCCACAGAGACTTCTCCACAGGTGAGCTGGG	420
Db	436	TGGGTGAAGTGAATACCATTTGACAGCCACAGAGACTTCTCCACAGGTGAGCTGGG	495
QY	421	CGCGTCATGAAAATACACCGAGGTGCGAGCTTGGAGCTGTGTGCCGACGGGCTTC	480
Db	486	CGCGTCATGAAAATACACCGAGGTGCGAGCTTGGAGCTGTGTGCCGACGGGCTTC	555
QY	481	TACCTGGGCTTCACAGAGCTATGGGGGCGCATTGCCATCCATCCGCGTGGCTCTTAC	540
Db	556	TACCTGGGCTTCACAGAGCTATGGGGGCGCATTGCCATCCATCCGCGTGGCTCTTAC	615
QY	541	CGCAAGTCCCCCGCATCATCAGAAATGGCCCATCTTCCAGAAACCTCTCGGGGGCT	600

D	b	616	CGAAGGTGTCCTGGTGTGATCCAGAGGGGGGCTTCCAGAAACCTCTGTGGGAGCG	675
Q	y	601	GAGAGCACATCGTGTGTGTCGCCGGGGAGCTGTGATCCCAATGCGGAAGAGGTGAT	660
D	b	676	GAGAGCACATCTGTGTGTGGACCGGGGGAGCTGTGATCCCAATGCGGAAGAGGTGAT	735
Q	y	661	GTACCCATCAAGCTCTACTGTAAAGGGGGAGCGAGTGGTGTGGCCCATGGGCGCTGC	720
D	b	736	GTGCCATCAAGCTCTACTGTAAAGGGGGAGCGAGTGGTGTGGCCCATGGGCGCTGC	795
Q	y	721	ATGTGCAAGAGAGGCTTGTGAGACCGTTTGAATGAGCACCGTCTGCCAGTGTTCATCT	780
D	b	796	ATGTGCAAGCGGGGTATGATGTCGGTGGAGATGGGACCTGTGAGAGGCTGTGCCATCA	855
Q	y	781	GGGACTTTCAGAGCCCAACCAAGGGATAGAGCGCTTACCACTGTGCCATCAAGCGCG	840
D	b	856	GGGACTTTCAGAGCCCAAGAGAGATAGAGTGTTCATTGTCCATTAAACGCCGG	915
Q	y	841	ACCACCTTGTGAAGGGGGACCAACACTGTGTGCCGCAATGAGCTACTACAGAGACCTG	900
D	b	916	ACGACTTGTGAAGGGGGACCAACACTGTGTGCCGCAATGAGCTACTACAGAGACCTG	975
Q	y	901	GACCCCTGTGACATGCTTCGACAAACCATCCCTCCGGGGCCAGGCTGTATTTCCAGT	960
D	b	976	GACCCCTGTGACATGCTTCGACAAACCATCCCTCCGGGGCCAGGCTGTATTTCCAGT	1035
Q	y	961	GTCATGAGACCTCCCTATGCTGTGAGTGAACCCCTCCGGGGAGTCCGGAAGCCGGAAG	1020
D	b	1036	GTCATGAGAACCTCCCTATGCTGTGAGTGAACCCCTCCGGGGAGTCCGGAAGCCGGAAG	1095
Q	y	1021	GACCTGTGTACACATCATCTGTGCAAGAGCTGTGCTGGGCGGGGGTCTGTGACCCGC	1080
D	b	1096	GATCTGTGTACACATCATCTGTGCAAGAGCTGTGCTGGGCGGGGGTCTGTGACCCGC	1155
Q	y	1081	TGCGGGGCAAAATGTACAGTACAGACGACGACGCTAGAGCTGACGAGCACCAATTAC	1140
D	b	1156	TGCGGGGCAAAAGTGTAGATTTGGCCCGACGCGACGCTGAGGAGCTGTGACATAC	1215
Q	y	1141	ATCAGTACCTGTGTGCGCCACACCCAGTACACCTTGAGATCCAGCTGTGAGAGGCTT	1200
D	b	1216	ATCAGTACCTGTGTGCGCCACACCCAGTACACCTTGAGATCCAGCTGTGAGAGGCTT	1275
Q	y	1201	ACTGACCAAGGCCCTTCTGCGCTCAGTTGCGCTCTGTAAATATCAACCAACCAAGCA	1260
D	b	1276	ACCGACCAAGGCCCTTCTGCGCCACAGTTTGTGATCAGTAAATATCAACCAACCAAGCT	1335
Q	y	1261	GCTCCATCGGAGTGTCCATCATCATCATGAGTGAAGCGGACCGTGGAGACATTAACCTG	1320
D	b	1336	GCTCCATCGGAGTGTCCATCATCATCATGAGTGAAGCGGACCGTGGAGACATTAACCTG	1395
Q	y	1321	TGCTGTGCCAGCGGAGCAAGCCCAATGCGGTATCTCTGACTATGAGTGTGACATCTAT	1380
D	b	1396	TGCTGTGCCAGCGGAGTGAATTTAAATTAACAGAGTGAAGAGGCCCAACCAACTGTGAA	1455
Q	y	1381	GAGAAGAGTGTGTAGTAAACAGCCAGCCATTAAGGCCCCCAACCAAGCGTCAAG	1440
D	b	1456	GAGAAGAGTGTGTAGTAAATTTAAATTAACAGAGTGAAGAGGCCCAACCAACTGTGAA	1515
Q	y	1441	G-----GCTCAAGCGCGGCCCATCTATGCTTCCAGGTGGGGACGCACTGTGCA	1494
D	b	1516	GTCGAAACCTCAAGGTGCGACCATCTATGCTTCCAGGTGGAGCACTGACCTGGCT	1575
Q	y	1495	GCGTACGGGCGCTACAGCGGCAAGATGTACTTCCAGACCATGACAGAACCGGATCCAG	1554
D	b	1576	GCGTACGGGCGGATATAGTGAAGATGTACTTCCAGACCATGACTAAAGCGGATCCAG	1635
Q	y	1555	ACAAGATCCAGAGAGATGTGACCATCATGAGCTCTCGGCGCGCTGTGCTGTCTTC	1614
D	b	1636	ACAAGTGTCCAGAGAGATGTGACCATCATGAGCTCTCGGCGCGCTGTGCTGTCTTC	1695
Q	y	1615	CTCATGTGTGTGTGTATGCGCATGCTGTGTAC---AGACGGGGGTTTGAAGCTGCT	1671
D	b	1696	CTCATGTGTGTGTGTATGCGCATGCTGTGTAC---AGACGGGGGTTTGAAGCTGCT	1751
Q	y	1672	GACTCGAGTACACGAGACAACTGTCAACACTATACCAAGTGGCCACATTAACCCAGGATG	1731
D	b	1756	GACTCGAGTACACTACAAAGCTGTGCAAGCTATACCAAGTGGCCACATGTACTCAGGATG	1815
Q	y	1732	AAATCTACATGATCTTCCACTACAGAGACCCCAACAGAGCAATGGGGGATTTGGC	1791
D	b	1816	AAATCTACATGATCTTCCACTACAGAGACCCCAACAGAGCAATGGGGGATTTGGC	1875
Q	y	1792	AAAGAAATTAACATCTCTGTCAAAATTTAGACAGTGTATCGAGCAGGGAGTTTGGC	1851
D	b	1876	AAAGAAATTAATATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1935
Q	y	1852	GAGTGTGAGTGGCCACCTGAAGCTGCCAGGCAAGAGAGATCTTTGTGTGTGTGTGT	1911
D	b	1936	GAGTGTGAGTGGCCATCTCAAGCTTCCAGGAAAGAGAGATCTTTGTGTGTGTGTGT	1995
Q	y	1912	ACGTCATGCGGGCTTCACAGGAGAGACGCGGGGACTTCTGTGAGCGAAGCTTCATC	1971
D	b	1996	ACGTCATGCGGGCTTCACAGGAGAGACGAGAGGAGACTTCTGTGAGCGAAGCTTCATC	2055
Q	y	1972	ATGGCCAGTTTGACATCCCAACGTCATCCACTGAGAGGCTGTGTGTGTGTGTGTGTGT	2031
D	b	2056	ATGGCCAGTTTGACATCCCAACGTCATCCACTGAGAGGCTGTGTGTGTGTGTGTGTGT	2115
Q	y	2032	CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2091
D	b	2116	CCATCATGATCATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2175
Q	y	2092	AACGATGGGAGTTCACAGTATCATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2151
D	b	2176	AATGATGGGAGTTCACAGTATCATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2235
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D	b	2236	ATGAATGATCTGTGATATATATATATATATATATATATATATATATATATATATATAT	2295
Q	y	2212	GTCAAACACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2271
D	b	2296	GTCAAACACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2355
Q	y	2272	GATACCTGAGACCCACCTACACCAAGTGCCTGTGGGGGAAAGTTTCCCATTCGCTGGACA	2331
D	b	2356	GATACCTGAGATCCACCTACACCAAGTGCCTGTGGGGGAAAGTTTCCCATTCGCTGGACA	2415
Q	y	2332	GCCCCGGAAGCAATCCAGTACCGGAGTTCACCTGCGGACATGATGTGTGTGTGTGTGT	2391
D	b	2416	GCCCCGGAAGCAATCCAGTACCGGAGTTCACCTGCGGACATGATGTGTGTGTGTGTGT	2475
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DG 946 GACCTGTGACATGCCATGCCACCACTCCCATCTGCCCCCACTCCGTGATCTCCAGT 1005  
QY 961 GTCAATGAGACCTCCCTCATGTGTGAGTGAACCCCTCCCGGAGCTCCGAGCCGAGAG 1020  
DB 1006 GTGAAGCAAACTCCCTCATGTGTGAGTGAACCCCAACAGAGTCTCGGGGGCCGGGAG 1065  
QY 1021 GACCTGTGCTACATATATCTGCAAGAGCTGTGGCTGGGGCCGGGGTCCCTGCAACCCG 1080  
DB 1066 GATCTGTGTATACATATATCTGCAAGAGCTGTGGCTGGGGCCGGGGTCCCTGCAACCCG 1125  
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RESULT 13  
LOCUS 115005 4097 bp DNA PAT 02-APR-1996  
DEFINITION Sequence 11 from patent US 5457048.  
ACCESSION 115005  
VERSION 115005.1 GI:1249913  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 4097)  
TITLE Pasquale, E.B. and Sajjad, F.G.  
Eph-related tyrosine kinases, nucleotide sequences and methods of use  
JOURNAL Patent: US 5457048-A 11 10-OCT-1995:  
FEATURES Location/Qualifiers  
Source 1..4097  
BASE COUNT 1014 a 1029 c 1087 g 967 t  
ORIGIN

Query Match 71.8%; Score 2127.6; DB 10; Length 4097;  
Best Local Similarity 82.7%; Pred. No. 0;  
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LOCUS Homo sapiens (clone FBK III 16) protein tyrosine kinase (NET PK) mRNA, complete cds.  
DEFINITION  
ACCESSION L40636.1 GI:1100111  
VERSION L40636.1  
KEYWORDS NET PK gene; neuronal differentiation; protein-tyrosine kinase.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3871)  
AUTHORS Tang,X.X., Biegel,J.A., Nycum,L.M., Yoshioaka,A., Brodeur,G.M., Pleasure,D.E. and Ikegaki,N.  
CDNA cloning, molecular characterization, and chromosomal localization of NET(PHPT2), a human EPH-related receptor protein-tyrosine kinase gene preferentially expressed in brain  
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96115594

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Oy 1679 AGTACAGGACAGCTGCAACACTACACAGTGGCCCATMAACCCAGCATGAAGTCT 1738
Db 1941 TGTACAGGATTAAGCTCCAGCATTTACAGACAGCGGAGGCTCCCAAGGATTAAGTCT 2000
Oy 1739 ACATCGATCTTTCACCTAGAGAGACCCCAACAGAGAGTGGGAGTGTCCAGAGAAA 1798
Db 2001 ACATTTGACCCCTTACCTTAAGAGAGATCCCAAGCAAGTGTGCGGAGTGTCCAGAGAG 2060
Oy 1799 TTGACATCTCTGTGTCAAAATTTGAGCAGGTGTATGAGAGGAGGAGTGTGGGAGTCT 1858
Db 2061 TTGATGTATCTTTTGTGAAAATTTGAAGAGTCTATCGAGAGAGGAGTGTGGAGAGTGT 2120
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Db 2121 ACAAGGGGCGTTTGAACCTGCGCAGGCAAGAGGAAATCTTACGTGGCATCAACAGCTCA 2180
Oy 1919 AGTCGGGCTACAGGAGAAACAGCGCGGAGCTTCTGAGCGAAGGCTCATCATAGGCGC 1978
Db 2181 AGGAGAGGCTACTGGAGAAAGCAGCTGCGGACTTTCTGAGTGAAGCGGAGCATATGCGGC 2240

Oy 1979 AGTTCAGACATCCCAAGTTCATCCACCTGGAGGGTGTGCTGACCAAGACACACTGTGA 2038
Db 2241 AGTTCAGACATCCCAAGTTCATCCACCTGGAGGGTGTGCTGACCAAGACACTGTGTGA 2300
Oy 2039 TGATCATCACCGAGTTCATGAGAAATGGCTCCCGAGACTCTTCTCTCGGCAAAAGCATG 2098
Db 2301 TGATCATCACAGAGTTCATGAGAAATGGCTTCATGAGTTCCTTCTCTCGGCAAAATGACG 2260
Oy 2099 GGCAGTTCACAGTATCATCAGCTGTGGGATGCTTCCGGGCAATGCGAGCTGGATGAAGT 2158
Db 2361 GGCAGTTCACAGTATCATCAGCTGTGGGATGCTTCCGGGCAATGCGAGCTGGATGAAGT 2420
Oy 2159 ACTGCGAGACATCAATATGTTACCGTACCGGCTGTGCGGCAATGCTGTGTGAACA 2218
Db 2421 ACTGCGTGTAGATGAATTAATGTGATCTGAGACCTGGCTGTGAGAAACATTTGTGTGAACA 2480
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Db 2541 CAGATCCGACCTTACACAGTGGCTGTGGCGGAAAGTCCCTGTGAGATGAGACAGCTCAG 2600
Oy 2339 AAGCATCCAGTACCGGAATTCACCTGGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGA 2398
Db 2601 AAGCATCCGCTTACCGGAATTCACCTGGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGA 2660
Oy 2399 TGTGGAGTGTATGCTTATGTGGAGCGGCTTACTGTGGAGCATGACCAACAGATGTAA 2458
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Db 3141 TCAGATTAAGTCACTGACCAACGCAATGAGTGA 3177
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Search completed: July 10, 2001, 17:59:33  
Job time: 10295 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 16:52:23 ; Search time 195.92 Seconds

(without alignments)  
9492.878 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962  
Sequence: 1 CTCGTCGCCGCCGTCGAAGA.....CCAAAGCCCCCCTCTGC 2962

Scoring table: IDENTITY\_NUC  
Gapext 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2962	100.0	2962	16	AA02946
2	2923.4	98.7	3768	21	AA088548
3	2897.2	97.8	3151	21	AAA09322
4	2884	97.4	3949	21	AAA88549
5	2498	84.3	3105	18	AA084528
6	2496.4	84.3	3105	16	AA07308
7	2187.2	73.8	4049	16	AA090660
8	2127.6	71.8	4097	16	AA090657
9	1651	55.1	4281	14	AA053471
10	1583.4	53.5	3751	15	AA062461
11	1581.6	53.4	3546	16	AA090656

12	1543.4	52.1	3591	16	AA090658
13	1526.4	51.5	4027	16	AA090972
14	1526.4	51.5	4027	16	AA090982
15	1520.8	51.3	2982	16	AA090971
16	1469.6	49.6	3133	16	AA090652
17	1196.8	40.4	3776	16	AA090655
18	1075	36.3	3969	16	AA090658
19	1073.4	36.2	4290	16	AA090659
20	1073.4	36.2	4290	17	AA090661
21	1073.4	36.2	4290	18	AA090662
22	1072.4	36.2	4290	18	AA090663
23	1067.2	35.9	4290	17	AA090664
24	1037.2	35.0	3116	16	AA090665
25	1035.6	35.0	3348	16	AA090666
26	992.8	33.5	3254	16	AA090667
27	956.8	32.3	3162	16	AA090668
28	949.4	32.1	2820	16	AA090669
29	943.8	31.9	4304	17	AA090670
30	917.6	31.0	3300	21	AA090671
31	912.8	30.8	3149	21	AA090672
32	907	30.6	4529	16	AA090673
33	906.4	30.6	3132	14	AA090674
34	869	29.3	3906	20	AA090675
35	800.8	27.0	4022	19	AA090676
36	799.2	27.0	3673	19	AA090677
37	743	25.1	3367	21	AA090678
38	735.4	24.8	1509	14	AA090679
39	723	24.4	2170	20	AA090680
40	697.2	23.5	3592	20	AA090681
41	661.2	22.3	3059	16	AA090682
42	629.6	21.3	3056	16	AA090683
43	605.2	20.4	3125	16	AA090684
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45	564	19.0	4322	19	AA090686

#### ALIGNMENTS

RESULT 1	AA02946	standard; cDNA; 2962 BP.
ID	AA02946	standard; cDNA; 2962 BP.
AC	AA02946	
DT	16-APR-1996	(first entry)
DE	EPH-like receptor protein tyrosine kinase HEK5 cDNA.	
KW	EPH-like receptor protein tyrosine kinase; PTK; HEK5;	
KW	human eph-like kinase; therapy; diagnosis; antibody; vector; ss.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	1..2913
FT		/*tag= a
PN	W09528484-A1.	
PD	26-OCT-1995.	
PF	14-APR-1995;	95WO-US04681.
PR	15-APR-1994;	94US-0229509.
PA	(AMGE-) AMGEN INC.	
PI	Fox GM, Jing S, Welcher AA;	
DR	WPI, 1995-373799/48.	
DR	P-PSDB; AAR85089.	
XX		

EPH-related PTK Ce  
Protein p140 cDNA  
Protein p140 cDNA  
Protein p140 cDNA  
EPH-related PTK Ce  
EPH-related PTK Ce  
Human non-differen  
Coding sequence fo  
Receptor-type tyro  
PTK gene HPRK5. H  
Receptor type tyro  
EPH-like receptor  
Protein tyrosine-k  
EPH-related PTK Ce  
EPH-like receptor  
EPH-related PTK Ce  
Mouse developmenta  
cDNA encoding a hu  
EPH-like receptor  
HEK coding sequenc  
Rat receptor tyros  
Human receptor typ  
Human thymus recep  
cDNA encoding huma  
PTK gene B1. Ratt  
Human normal ovar  
Rat receptor tyros  
EPH-related PTK Ce  
EPH-related PTK Ce  
EPH-related PTK Ce  
Rat REK7 cDNA. Ra  
Mouse Bsk receptor

PT New nucleic acid encoding Eph-like receptor tyrosine kinase(s)  
PT and related vectors, host cells, proteins, antibodies etc., used  
PT diagnostically and therapeutically to modulate receptor activation  
PT or prodn.

XX Claim 1; Page 41-45; 133pp; English.

CC cDNAs (AA02946-49) coding for a novel human Eph-like receptor protein  
CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (AA085089-92),  
CC respectively, were isolated from a human fetal brain cDNA library using  
CC a directed PCR approach with primers (see AA02960-61) based on conserved  
CC regions of receptor PTKs and Eph-like receptor PTKs. HEK5, HEK7 and HEK8  
CC show extensive homology to the catalytic domain of chicken Eph-like  
CC receptors Cdk5, Cdk7 and Cdk8. HEK11 shows no homology to any known  
CC Eph-like receptor. The isolated cDNAs are used for prodn. of  
CC recombinant HEKs and chimeric receptors, in hybridisation assays, and  
CC to detect abnormalities in HEK receptor genes.

XX Sequence 2962 BP; 654 A; 914 C; 827 G; 567 T; 0 other;

Query Match 100.0%; Score 2962; DB 16; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGCTCGCGCGCGTGGAGAAACGCTAATGACTCCACTACAGGACTGTGAGCTGGAC 60  
OY 61 TGGATGTGTCATCTCTCATCAGGTTGGAGAGAGTGAAGTGGCTACGATGAGAACATGAA 120  
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OY 121 ACGATCCGACCTACAGGTTGTCAGAGCTGTTGATGATCAAGCCAAACAACTGGGTAGG 180  
DB 121 ACGATCCGACCTACAGGTTGTCAGAGCTGTTGATGATCAAGCCAAACAACTGGGTAGG 180  
OY 181 ACCAAGTTTATCCGCGCGCTGGGCGCCACCGCATCCAGTGAATGAATGTTTCGGTG 240  
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DB 961 GTCAATGAGACTCTCCCTGATCTGAGTGAACCCCTCCCGGAGCTCGGAGGCGGAG 1020  
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Db 2881 cagatgaaccagattcagttctgtaggtttgacattcaccctgcctgcctcactcttc 2940
QY 2941 CTCGAAGCCCCGCCCTCTGC 2962
Db 2941 ctccaagccccgcctcctctgc 2962

RESULT 2
AAA8548
ID AAA8548 standard; cDNA; 3768 BP.
XX
AC AAA8548;
XX
DT 22-JAN-2001 (first entry)
XX
DE Human CASB616 cDNA.
XX
KW CASB616; EPHB2; ERK; EPH3; EPH3T3; DRT; HEK5; EPHB2V;
KW receptor protein tyrosine kinase; human; antigen; colon cancer;
KW ovary cancer; tumour; autoimmune disease; vaccine; gene therapy;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 105..306
FT FT /*tag= a
FT /transl_except= (pos:2973..2975,aa:Leu)
PN MO200053216-A2.
XX
PD 14-SEP-2000.
XX
PF 28-FEB-2000; 2000MO-BE01587.
XX
PR 05-MAR-1999; 99GB-0005124.
XX
PA (SMRK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Vinals De Bassols YC;
XX
DR WPI: 2000-587384/55.
XX
P-PSDB; AAB19590.
XX
PT Vaccine composition for treating ovarian and colon cancer, comprises
PT CASB616 polypeptides, polynucleotides or antigen presenting cells
PT expressing the polypeptides
XX
PS Claim 3; Page 40-41; 57pp; English.
XX
CC The present sequence is that of cDNA coding for human CASB616 (see
CC AAB19590), a member of the EPH and EPH-related family of receptor
CC protein tyrosine kinases. CASB616 is also known as EPHB2, ERK,
CC EPH3, EPH3T3, DRT, HEK5 and EPHB2V. CASB616 polypeptides and
CC polynucleotides are important immunogens for specific prophylactic
CC or therapeutic immunization against tumours, especially colon
CC cancer (claimed) and ovarian cancer. They are specifically
CC expressed or highly over-expressed in tumours compared to normal
CC cells and can thus be targeted by antigen-specific immune
CC mechanisms leading to destruction of the tumour cells. They can
CC also be used to diagnose the occurrence of tumour cells. Their
CC inappropriate expression can also cause an induction of autoimmune
CC responses, which can be corrected through vaccination using the
CC CASB616 polypeptides or polynucleotides.
XX
SQ Sequence 3768 BP; 872 A; 1129 C; 1058 G; 709 T; 0 other;

Query Match 98.7%; Score 2923.4; DB 21; Length 3768;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2956; Conservative 0; Mismatches 6; Indels 9; Gaps 2;
QY 1 CTGCTCGCCGCGTGGAGAAACGCTAATGAGACTCCACTACAGCAGCTGAGCTGGGC 60

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Db 147 ctgtctgcgcgcgtggaagaacgtactatgactccactacagcagctgctgagcttgcc 206  
QY 61 TGGATGCTGATCTCTCCATCAGGGTGGGAAGAGTGAGTGGCTACGATGAGAACATGAAC 120  
Db 207 tggatggtgcatctccatccatcaggttggaaagagtgagtggtctacgatagaacaatgac 266  
QY 121 ACGATCCCGCAGTACCCAGTGTGCAACGCTGTTTGATGATCAACCCAAACAACTGGCTACG 180  
Db 267 acgatccgcacgtaccaggtgtgcaacgtgttggatcaagccagaaacactggtacgag 326  
QY 181 ACCAAGTTTATCCGGCGCGCTGGGGCCACCGCATCCAGTGGAGATGAAGTTTTCGGTG 240  
Db 327 accaagttaaccggtgcgcgtggtggccacgcgtccacgtcgaatgagagatgaatttcggtg 386  
QY 241 CGTGACTGCACAGCATCCCAACGCGCTGCTGCTCTCCAAAGAGAGACCTTCAACTAT 300  
Db 387 cgtgactgcagcagatcccacagcgtgctgtgctctgcaagagaaacttcaactctat 446  
QY 301 TACTATGAGGCTGACTTTGACTCGGCGCACCAAGACTTCCCACTGGATGGAGATGCA 360  
Db 447 tactatgaggtgacttgacttgactcgcgcacaaagaccttcccacactggtatgagaatcca 506  
QY 361 TGGGTGAAGTGTGATATCATTGCAAGCCGACGAGAGACTTCTCCAGAGTGGACCTGGGTGC 420  
Db 507 tgggtgaaagtgtgataccattgacgtcagcgcagcagagacttctcccaagtgtgacctgtg 566  
QY 421 CGCGTATGAAATATCAACACGAGGTGCGGAGCTTGGACCTGTCTCCGACGGCGCTTC 480  
Db 567 cgcgtcatgaaataataaacacgaggttgcgagcttcggaacctgtgtccgcgcgcgtcttc 626  
QY 481 TACCTGGGCTTCCAGAGACTATGCGCGCTGCAATGCTTCATCGCGCTGCTGCTTCTTAC 540  
Db 627 tactctgagcttcccgagatatagtggtcgtgcatgtccctcatccgcgtgctgtcttctac 686  
QY 541 CGCAAGTCCCCCGCATATCCAGAAATGCGCATTTTCCAGAAACCCTGTGGGGGCT 600  
Db 687 cgcgaagtccccgcgcatcatccagaaatggtgcacatcttccagaaacctgtcggggct 746  
QY 601 GAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db 747 gaggagcaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 806  
QY 661 GTACCCATCAAGCTCTACTGTATACGGGAGCGGAGTGGTGGTGGTGGTGGTGGTGGTGG 720  
Db 807 gtacccatcaagctctactgtataaagggtgagcgtggtgtgtgtgtgtgtgtgtgtgtgt 866  
QY 721 ATGTGCAAGAGCGCTTGAAGGCGCTTGAGAAATGGCACCGTGTGCGAGGTTTGCATCT 780  
Db 867 atgtgcaagcaggtctcgaggtgtgagaaatggtgtgtgtgtgtgtgtgtgtgtgtgtgt 926  
QY 781 GGGATTTCAAGGGCCAAACCAAGGGGATGAGGCTGTACCCATGTCATCAACAGCGGG 840  
Db 927 gggatcttcaaggtccaaacaaagggtgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 986  
QY 841 ACGACTTGTGAAGGGGCCACCAACTGTGTGTGCGCAATGGCTACTACAGACAGACCTG 900  
Db 987 accaacttgaagggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1046  
QY 901 GACCCCTTGAGATGCTCTGCAACACATCCCTCCGCGCCCAAGGCTGTGATTTCCAGT 960  
Db 1047 gaccccttgagatgtccttgcaacaacatcccttcgcgcgcgcgcgcgcgcgcgcgcgcgc 1106  
QY 961 GTCAATGAGACCTCCCTATGCTGAGTGGAGCCCTCCCGGAGTCCGGAGCGGAGAG 1020  
Db 1107 gtcaatgagacctccctcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1166  
QY 1021 GACCTGTCTACACATCATCTGCAAGAGCTGTGCTGGGCGGGGAGTCCGTCAACCGCG 1080  
Db 1167 gacctgtctacaacatcatctgtcaagagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1226  
QY 1081 TGGCGGGCAATGTACAGTACGACACGACGCTAGGCTGTACGAGCGACGCAATTAC 1140  
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Db 1227 tgcggggacaatgtatacagtaacacacgcagctaggtgcctgaccaggtccacgtattac 1286  
QY 1141 ATCATGTACCTGTGTGCCCCACACACCCAGTACACCTTCCGAGATCCAGGCTGTAAACGGCGTT 1200  
Db 1287 atcatgtacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1346  
QY 1201 ACTGACCGAGAGCCCCCTTCCGCTCAGTTCGCTGTGTGAACATCAACCAACCAACGACGA 1260  
Db 1347 actgacccagagcccccttctgctcctagttgtgctctgtgtgaacatcaccaaccaggtgca 1406  
QY 1261 GCTTCATGAGGAGTTCATCATGATGATGAGTGAAGCCGACCGCTGGAGACATTAACCTG 1320  
Db 1407 gctccatcgcaggtgttccatcatcatcatcaggtgtgagccgaccgtgtgacgaattaccctg 1466  
QY 1321 TCGTGTGCTCCAGCGGACCGACCGCAATGGCGTGTGATCCGATGATGATGATGATGATGAT 1380  
Db 1467 tctgtgtccaggtccaggtccaggtccaggtccaggtccaggtccaggtccaggtccaggtccag 1526  
QY 1381 GAGAAGAGAGCTCAGTGAATGATACAGCCACAGCATTAAGCCGACCAACAGCGGTCAAC - 1439  
Db 1527 gagaagagagctcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1586  
QY 1440 -----GGGCTTCAAAACCGGCGCATGTATGTCTTCCAGGTGCGGCGACGACTGTGCA 1494  
Db 1587 gtgcagggcctcaaaagccgcgcgtcatctatgtcttccaggtgtgcgcgcgcgcgcgcgcgc 1646  
QY 1495 GGCTACGGGGCGCTACAGGGGAGATGATCTTCCAGACATACAGAGCGAGCGAGTACAG 1554  
Db 1647 ggcctacggggcgtacagagagagagagagagagagagagagagagagagagagagagagagag 1706  
QY 1555 ACAAGCATCCAGAGAGAAATGGCCATCATCGGCTCCTCGGCGCTGCGCTGTCTTC 1614  
Db 1707 acaagcatccaggaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1766  
QY 1615 CTCATTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1671  
Db 1767 ctcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1826  
QY 1672 GACTCGAGTACAGGAGACGAGCTGACACACTGACAGTGGCGCATTAACCCAGGACATG 1731  
Db 1827 gactcggaggtacaggtacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1886  
QY 1732 AAGATCTACATGATCTTTTCACTTACAGAGACCCCAACGAGGACGTGCGGAGTTTGCC 1791  
Db 1887 aagatctacatgacttcttccatcctacagagagcccaagagcaggtgcggaggtgtgtgtgt 1946  
QY 1792 AAGGAAATTTGACATCTCTGTGTCAAAATTTGACAGGTGATCGGAGCGAGGAGTTTGGC 1851  
Db 1947 aaggaaatttgacatctctgtgtcaaaatltgagcaggtgtgtgtgtgtgtgtgtgtgtgtgt 2006  
QY 1852 GAGGTCTCAGTGGCCACCTGAAAGCTGGCAGGCAAGAGAGATCTTGTGGCATCAAG 1911  
Db 2007 gagggtctcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2066  
QY 1912 ACGCTCAAGTGGGCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1971  
Db 2067 acgcctcaaggtcgggtacagagagagagagagagagagagagagagagagagagagagagag 2126  
QY 1972 ATGGGCGAGTTTGACATCCCAACGTCATCCACTGTGAGAGGAGGTGTGTGACCAAGAGACA 2031  
Db 2127 atgggccaagtttgcacatcccaaggtcatccacccgtggagaggtgtgtgtgtgtgtgtgtgt 2186  
QY 2032 CCTGTGATGATCATCAGAGATTGATGAGAAATGGCTCCTTGAGACTCTTTTCTCCGGCA 2091  
Db 2187 cctgtgtatgatcatcacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2246  
QY 2092 AACGATGGGCAATTACAGATCATCCAGCTGGTGGGCAATGCTTGGGGCAATCCGACACTGGC 2151  
Db 2247 aacgatgggcaatttaccaggtcatccaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2306  
QY 2152 ATGAGTACCTGTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2211  
Db 2307 atgaagtacctgtgcagacatgtacatgttccacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2366  
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OY 2212 GTCAACAGCAACCTGCTGTGCAAGGTGTGAGACTTTGGGCTCTCAACGCTTTCTAGAGAC 2271
    |||||||
Db 2367 gtcaacagcaacccggtctgcaaggtgtcgaacttggcctcctcaagcttctctagagac 2426
OY 2272 GATACCTCAGACCCACCTACACAGTGCCCTGGGCGGAAAGTTTCCCATCCGCTGGACA 2331
    |||||||
Db 2427 gatccctcagcccccaactcaacagtgccctggcgaaagatccccaaccgctggaca 2486
OY 2332 GCCCGGAAGCCATCGATACCGGAAGTTCACTCGGCATGATGTGTGAGCTAGCGC 2391
    |||||||
Db 2487 gcccggaagcaccacccagtaaccggaagttcaaccctcgccagtgatgtgtgagtaagc 2546
OY 2392 ATTGTCAATGTGGAGATGATCTCTATGGGAGAGCGCCCTACTGTGAGATGACCAACAG 2451
    |||||||
Db 2547 attgtcaatgtggagatgattctctatgggagagcgccctctggaatgacccaacag 2606
OY 2452 GATTAATCAATGGCATTTGACAGAGCATATGGCTGGCAGCGCCCATGAGATGGCCGAGC 2511
    |||||||
Db 2607 gatatacaatgcatatgagcaggaactatcgctgcacccgccaatggactgcgagc 2666
OY 2512 GCCCTGCACCAATCTATCTGTGAGCTGTGGCAGAAGACCGCAACACCGGCCCAAGTTC 2571
    |||||||
Db 2667 gccctgcaccaactcatgctgactgttgagagaagaccgcaaccgcccgaagttc 2726
OY 2572 GGGCAATTGTCAACAGCTAGAGAAATGATATCCGCAATCCCAACAGCTCAAGCCATG 2631
    |||||||
Db 2727 gggcaaatgtcacaagctagagaagatgacgcgaatcccaacagctcaagcattg 2786
OY 2632 GCGCCCTCTCTCTGTGGCATCAACCTCGCTGTGGACCGACAGATCCCGACTACAC 2691
    |||||||
Db 2787 gcgcctctctctctgtgcatcaactcgcgtctgtgagccgcaagatcccgactacac 2846
OY 2692 AGCTTTAACACGGTGAACAGATGGCTGTGAGGCCATCAAGATGGGCAAGTCAAGAGAGC 2751
    |||||||
Db 2847 agctttaacacggtgagcaggtgtgagccatcaagatgggagcagtaagaagagc 2906
OY 2752 TTGGCCAAATGCGGCTTCACTCTCTTGTGAGCTGTGTCTAGATGATGAGAGACATT 2811
    |||||||
Db 2907 ttcgccaatgcccgtctcaactcctcttgacgtctgtctcagatgagatgagagacat 2966
OY 2812 CTCGGGTTGGGATCACTTTGGCTGGCCACAGAAAAAATCTGAGACAGATATCAGATG 2871
    |||||||
Db 2967 ctccgggttgggtcactcttggtcgcacccagaaaaaactctgacagatcccaagtg 3026
OY 2872 ATGGGGGCGAGATGAACAGATTCACTGTGTGAGGTTTGACATTCACTGCTCGCT 2931
    |||||||
Db 3027 atggggcgagatgaacagattcagtcgtgtgaggttttgacattcaactcgtcgtc 3086
OY 2932 CACCTTCTCTCCAGGCCGCCGCCCTCTGCG 2962
    |||||||
Db 3087 caccttctctcagagcccgccccctctgc 3117

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RESULT 3  
AAA09322 standard; DNA; 3151 BP.

XX AAA09322;  
XX 10-AUG-2000 (first entry)  
XX Human cancer associated antigen precursor DNA, clone NY-REN-47.  
XX renal cancer; cancer associated antigen precursor; diagnosis;  
XX cytosolic; ERK tyrosine kinase; ss.  
XX Homo sapiens.  
XX MO200020587-A2.  
XX 13-APR-2000.  
XX

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PF 04-OCT-1999; 99NC-U522873.
XX
PR 05-OCT-1998; 98US-0166300.
PR 05-OCT-1998; 98US-0166350.
XX
PA (LUDWIG INST CANCER RES.
XX Obata Y, Gout I, Tureci O, Sahin U, Pfreundschuh M, Scanlan MJ;
PI Stockert E, Chen Y, Old LJ, Jager E, Knuth A;
XX WPI; 2000-303774/26.
XX
PT Preventing, diagnosing and/or treating disorders associated with
PT abnormal expression of human cancer associated antigens
XX
PS Claim 57; Page 93-94; 121pp; English.
XX
CC AAA09321-45 were isolated by SEREX screening from a renal cancer
CC cell line 1973/10.4. Homology searching revealed that these clones
CC correspond to known genes. The present sequence has identity with the
CC ERK tyrosine kinase gene. The genes encode cancer associated antigen
CC precursors. These gene products are useful in methods for preventing,
CC diagnosing and/or treating disorders, especially cancer, associated with
CC abnormal expression of human cancer associated antigens. The method
CC comprises contacting a sample from a subject with an agent that
CC specifically binds to the nucleic acid molecule or expression product
CC (or fragment) complexed with a human leukocyte antigen (HLA) molecule
CC and determining the interaction between the agent and the nucleic acid
CC molecule or the expression product as a determination of the disorder.
XX
SQ Sequence 3151 BP; 707 A; 974 C; 874 G; 596 T; 0 other;

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Query Match 97.8%; Score 2897.2; DB 21; Length 3151;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 2934; Conservative 0; Mismatches 13; Indels 9; Gaps 2;

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OY 16 GAAGAAACGCTAATGAGCTCCACTACAGCAGTGTGAGCTGGCTGGATGTGATCTCT 75
    |||||||
Db 64 gaaagaaacgtataatgactcactcaagcagctcgtgagctggatgtgagctcct 123
OY 76 CCATTCAGGCTGGGAAGAGTGAATGAGTGTGAGTGAACATGAACAGATCCGACGTTAC 135
    |||||||
Db 124 ccatcaggtgtgaaaggtgagtgagtgactagaaabaacatgacacgacacgtac 183
OY 136 CAGGTGCAACGTTTGTGATCAGCAGACATCGCTGAGCTGGCTAGGCAAGTTATCCG 195
    |||||||
Db 184 caggtgtgcaacgttgtgactcaagcacaacacgtgtacgacaaagtataccgg 243
OY 196 CGCGTGGGGCCACCGCATCAAGTGAAGTATTTTCGCTGGCTGACTGCACAGC 255
    |||||||
Db 244 cgcggtggggccacacgcacacacgacacgagtgagtgagtttcggtgtgagtcagcagc 303
OY 256 ATCCCAAGCGTGCCTGCTGCTCTGCAAGAGACCTTAACCTATTATGAGCTGAC 315
    |||||||
Db 304 atcccaagcgtgcctgtcctcgaaggaagaccttaacctatatactatgagtgac 363
OY 316 TTGTACTCGGCAACAGACTTCCCACTGATGAGAAATCATGGGGAAGTGGAGT 375
    |||||||
Db 364 ttgtactcggcacacagaccttcccaactggaatgaaatccatggtgagtgagat 423
OY 376 ACCATTGCAAGCCAGAGAGCTTCTCCAGAGTGAGACTGGGTGGCCGCTCATGAATAATC 435
    |||||||
Db 424 accattgcaagccagagagcttcccaactggaatgaaatccatggtgagtgagat 483
OY 436 AACACGAGGTGGGAGCTTGGAGCTGTGCTCCGAGAGGGCTTCAACTGGCTTCAG 495
    |||||||
Db 484 aacacgaggtgggagcttggagctgtgctccgagagggcttcaactggtccttcag 543
OY 496 GACTATGGGCGGTGATGTCTCATGCGCTGCTGTCTTACCGCAAGTGGCCCGC 555
    |||||||
Db 544 gactatgggcggtgatgtctcatgctgctgtcttcttctacacgaagtgccccgcg 603

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OY 556 ATCATCCGAATGGGCGCATCTTCCAGGAAACCTGTGGGGGCGTGAGAGACATCGTGG 615
DB 604 atcaccagaatgycgcatcttccaagaaacccgtcggggccgagagcaacacgcgtg 663
OY 616 GTGGCTGCGCGGAGCGTGCATCCGCAATGGGGAAGAGTGTATGCCATCCATCAAGCTC 675
DB 664 gtggctgcgcgaggagctgcacgcgaatgsgaagagtgatgtaacctcaagctc 723
OY 676 TACTGTAAACGGGAGCGGAGTGTGCTGTCGCCATCGGGCGCTGCATGTGCAAGACGCG 735
DB 724 tactgtaaacgggagcgagtggtgtgcccacgcgcgtcgtacatgtgcataaagcaggg 783
OY 736 TTGAGGGCGCTTGAGAAAGGACGCGTGTGGAGGTTGGCTATCGCTTGGGACTTTCAAGGCG 795
DB 784 ttgagggcgcttgagaaagacgacgctgcgagaggtgttccactcgggaacttcaagccc 843
OY 796 AACCAAGGGGATGAGGCGCTGTACCCACTGTGCCATCAACAGCGGAGCACTTCTGAAGGG 855
DB 844 aaccaagggatgagggccgtacccacgtctccatcaacagcggagccactctgaagg 903
OY 856 GCCACCACTGTGTGTGCCGCAATGGCTACTACAGAGCAGACCTGACCCCTGGACATG 915
DB 904 gccaccaactgtgtctgcgcgcaatgtctactacagagaccttggaaccccttgacatg 963
OY 916 CCTGTGACAAACCATCCCTCCGCGGCCGAGGCTGTGATTTCCAGTGTCAATGAGACTTC 975
DB 964 cccgtgacaacacatccctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1023
OY 976 CTTCATGCTGTGAGTGAACCCCTCCCGGACTCCGAGCTCCGAGGCGGAGAGACTGCTTAACA 1035
DB 1024 ctcatgtgagtgagacccctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1083
OY 1036 ATCATCTGCAAAAGCTGTGTGCTGCGGCGGCGGCGGCTGTGACCCGCGGGGGAACAATGA 1095
DB 1084 atcatctgcaaaagctgtgtgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1143
OY 1096 CAGTACGACCAACGCGCAGTAGGCTGACCGAGCCAGCAGCATTTACATCAGTACGCTGTG 1155
DB 1144 cagtaacgacccaacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 1203
OY 1156 GCCCACACCCAGTACACCTTGCAGATCCAGGCTGTGAACGGGTTACTACCAAGAGCCCG 1215
DB 1204 gcccaacacccaagtaacacctcagatcagatcagatcagatcagatcagatcagatcag 1263
OY 1216 TTCTGCGCTCAGTGTGCTGTGGAACATCACACCAACGAGCAGCTCATCGGAGAGTG 1275
DB 1264 ttctgcgctcagttgcctcctgtgaaacatcaacacccaacgagcgtccatccgagatg 1323
OY 1276 TCCATCATGCATCAGGTGAGCGGACCGACCGTGGAGACGATTACCCCTGTGTGCCAGCG 1335
DB 1324 tccatcatgcatcaggtgagcgcgacgctggaagacattaccctgtcgtgtccagcca 1383
OY 1336 GACCAAGCCCAATGGCTGATCCTGGACTATGAGCTGATATAGAGTATATAGAGTCT 1392
DB 1384 gaccagcccaatggcgtgactcctgagactatgagctgagactatgagagagagagctc 1443
OY 1393 AGTGATTAACAGCGCCAGAGCATAAAAGCGCCACCAACAGGCTAC-----GGGCTTC 1446
DB 1444 agtgatlaaacgcccacacataaaaagcccacacacacggtcaccgltgcagggcctc 1503
OY 1447 AAAGCGGCGGCATCTATGTCTTCCAGGTGCGGGACGCACTGTGGCAGGCTTACGGGCGC 1506
DB 1504 aaagcgcgccatctatgttcttcaggtgctgagcagcgcgtgacggtctacgagcgcg 1563
OY 1507 TACAGCGGCAAGATGTACTTCCAGACCATGACAGAAAGCGAGTACCAAGACATCCAG 1566
DB 1564 tacagcggaagatgtacttccagacatgacagagccgatatacagaacaaacatcccg 1623
OY 1567 GGAAGTATGCACTCATCATCGGCTCTCGGGCGGCGGCTGTCTTCCATGTGCTGTG 1626
DB 1624 ggaagatgtccactcatcactcgtcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1683
OY 1627 GTTGTATCGGCATCGTGTGTAACAGACGGGGGTTTGAAGCTGCTGATCGAGTACAGC 1686

DB 1684 gtgtcatcgcatcgtgtgttaacagacgggggtttgagcgtgtcgtacgtcgagtaacg 1743
OY 1687 GACAAGCTGTCAACACTTACACCAATGTGGCCACTTAACCCCAAGGCATGAAGATATACATGAT 1746
DB 1744 gacaagctgtcaaaccttaacacagtggtgcacatgacacccaagatgaatatacactcgtat 1803
OY 1747 CCTTACCTACGAGCAGCCCAACAGAGGACATGCGGAGTGTGGCAAGAAATTGACATC 1806
DB 1804 ccttcaacctacgaggaacccaagagcagtgcggggtttgccaaagaaattgacatc 1863
OY 1807 TCCGTGTCAAAATTTGACAGGTGATCGAGACGAGGAGTTTGGCGAGCTGTCAAGTGGC 1866
DB 1864 tccgtgtcaaaatttgacagtgatcagagcaaggaggtttgagcaggtgtcgcagtgc 1923
OY 1867 CACCTGAAGCTGCCGAGGAGAGAGAGATCTTTGGGCATCAAGACCTCAAGTCGGGC 1926
DB 1924 cactgaagctgcccaggaagagagatcttctgtgcacataaagacctaagtcgagc 1983
OY 1927 TACAGGAGAAAGCAGCGCGGACTTCTGAGCGAAGCCTCATGAGGCGAGTTGAGC 1986
DB 1984 tacaggaagaagcagcgccgagacttccctgagcgagcctccatcatgtggccaagtgcag 2043
OY 1987 CATCCCAAGCTATCCACCTGAGGCTGTCTGTGACCAAGAGCAGACCTGTATGATCATC 2046
DB 2044 catcccaagctatccacacttgagaggtgtcgtgaccaaagacacccgtgatgatc 2103
OY 2047 ACCGAGTTCATGAGATAGGCTCCCTGAGACTCTTTCGCGCAAAAGATGGGAGTTTC 2106
DB 2104 accgagttcatggaagaaagtgccctcgactctcttccgcgcaaaagatgagagatc 2163
OY 2107 ACAGTATCCACAGTGTGGGATGCTTGGGGCATGCGAGCTGCGATGAATGACTGTGCA 2166
DB 2164 acagtaatccacgtgtgtgtgagacgtcttcggtgacatcgacgtgcatgaatcctgcga 2223
OY 2167 GACATGAGACTATGTTTACCGGTATCCTGGCTGCCCAACATCCTGTGTAACGCAACCG 2226
DB 2224 gacatgaactatgttaccgtgactgctgcgcgcaaatcctgtcaacagcaacgtg 2283
OY 2227 GGTGTCAAGGTGTGAGTCTTGGGCTTCACGCTTTCATGAGAGAGATACCTCAGACCC 2286
DB 2284 gttctgaaggtgtgtgacttgggtctctcaagcttctcagaagatatacctcagacccc 2343
OY 2287 ACCTACACCAAGTCCCTGGGGGAAAATTGCCCATTCGCTGACAGACGCCCGGAAACCATC 2346
DB 2344 acctaacacagtgcccttggcggaagatcccatcgcgttgagacgcccggaaacatc 2403
OY 2347 CAGTACCGGAAGTTACCTCGGCGAGTGAATGTGAGCTACGGCATTTGTCATGTGGAG 2406
DB 2404 cagtaacggaagttcacctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2463
OY 2407 GTGATGTCTATGGGAGGCGGCTTACTGGGACATGAGACACAGAGATGAATCAATGCC 2466
DB 2464 gtgatgtctatgggagggagggccctacttggaatgacacacagatgtaataatgtgc 2523
OY 2467 ATTGAGCAGACTATCGGCTCCACCGCCCATGAGTGTGCCGAGCGCCTTGACCAACTC 2526
DB 2524 attgagcagactatcgtgtgcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2583
OY 2527 ATGCTGAGTGTGGTGAAGAGACGCAACCGGCGCCAAAGTGGGCCAAATTTGCAAC 2586
DB 2584 atgctgagtggttggtagaagacgcaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2643
OY 2587 ACGCTAGACAAGATGATCGCAATCCCAACAGCCTTAAAGCCATGGCGCCCTCTCTCT 2646
DB 2644 acgctagaacaagatgtatccgcaatcccaacagcctcaaaagccatgtggccctctctct 2703
OY 2647 GGCATCAACCTGCGCTGTGACCGCACGATCCCGGATACCAACAGCTTTAAACAGGAG 2706
DB 2704 ggcataacactcgctgtgtgagccgacgacatcccgataacacagccttataacagtg 2763
OY 2707 GACGATGGCTGAGGCGCATCAAGATGGGGGAGTACAAAGAGAGCTTGGCAATGGCGGC 2766
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QY	2035	GTGATGATGATCACCACAGTTCATGAGGAATAGGCTCCCTGGAGATCCCTTCTCCGGCAAAAC	2034
Db	2108	gtgatgcatcaccacaggtctcctcaggaagaaagctccctgagacctctctcccggaataac	2167
QY	2095	GATGGGAGATTCAACAATCATCCAGCTGGTGGGATCTCTCGGGGATCGCAGCTGGCATG	2154
Db	2168	gatgggagattcacacajcatccacagctcggvgagatgcttcggggatcgcagctgcatg	2227
QY	2155	AAGTAACTGGCAGACATGAATCTATGTTTCAACCGTGACCTGGCTGGCCGAACAATCCTGCTC	2214
Db	2228	aagtaacctggagacatgaaactatgtctaacacgtgacctggctggccggaacactccctgc	2287
QY	2215	AACAGCAACCTGGATCTCAAGAGTGTCGGAATTTGGGCTCTCAAGCTTCTTAGAGGACAT	2274
Db	2288	aacagcaacctggatctcagagatgtctcgaagcttggctcctcaagctctctctagaggat	2347
QY	2275	ACCTCAGACCCCACTTACACCAATGCCCTTGCGGCGAAATGTTCCCATCGCTGGACACC	2334
Db	2348	acctcagacccccaactcacaacagctgcctctgggcggaagaatcccatcgcgtcgacaagc	2407
QY	2335	CCGGAGGCATTCAGATCCGGAAGTTACCTCGCCGACAGATGATGTGGAGCTACGAGCAT	2394
Db	2408	ccggagagcatcaccagatcccggaagatccaactcgtccagtgatgtgtggagctcagagct	2467
QY	2395	GTCATGTGGAGAGTGATGTCCTATGGGGAGGGCCCTACTGGGACATGACCAACAGGAT	2454
Db	2468	gtcatgtggagagtgatgtcctatggggagggccctactgggacatgacccaacagat	2527
QY	2455	GTAATTCATGGCATTTAGACAGGACATACCGGCTGCGACCCGACATGGACATGCCGAGCGCC	2514
Db	2528	gtaaatcaatgcatcttgacagagactaacgctgcgcacacgcccacatggaatctgcggagcgc	2587
QY	2515	CTGCGACCAACTCATGTGAGACTGTTGGCACAAGACGCGACACCGGCGCCCAAGTTGCGC	2574
Db	2588	ctgcgaccaactcatgtctgagactgttggcacaagacgcgacacccgagcccaagctgcgc	2647
QY	2575	CAAAATTGTCAAACGCTTAGACAAAGATGATCCGATATCCCAACAGCTCTAAAGCATGGCG	2634
Db	2648	caaaattgtcaaacgcctagacaagatgatccgaatcccaacagcctcacaagccaatggcg	2707
QY	2635	CCCCCTCCCTGGCATCAACCTGGCCGCTGCTGGACGCGACGATCCCGCATACACAGC	2694
Db	2708	ccccctccctcttgcatcaaacctgcgcgtcgtagacgcgaatgcccgactcaaccgaac	2767
QY	2695	TTTAAACAGGATGACAGATGGGCTGGAGCCATCAAGATGGGGCAGTACAGAGAGCTTC	2754
Db	2768	tttaaacagtgatgacagatgggctggagcccatcaagatggggcagtagtacaagagagcttc	2827
QY	2755	GCCAAATGCCGGCTTCACTCCTTTGACAGCTGCTCAGATGATGATGGAGGACATTTCTC	2814
Db	2828	gccaaatgccggcttcacctcctcttgtagatgtgtctccagatgatgtgtagagacattctcc	2887
QY	2815	CGGGTTGGGGGTCACTTTGGCTGGGCGACACAAAAAAATCCTGAACAGTATCCAGGTGATG	2874
Db	2888	cgggttgggggtcacttttggctgggcgacacaaaaaaatcctgaacagtatccaggtgatg	2947
QY	2875	CGGGCGCAGATGAACACAGATTCAGTCTGTGGACG	2908
Db	2948	cgggcgagatgaaacagatctcgttgtgaggg	2981
RESULT 5			
AAT84528			
ID	AAT84528 standard; cDNA; 3105 BP.		
XX	AAT84528;		
AC			
XX	02-DEC-1997 (first entry)		
XX			
DE	Mouse Nuk tyrosine kinase cDNA.		
Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction; axonogenesis; neurodegenerative disease;			

KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW multiple sclerosis; amyotrophic lateral sclerosis;  
 KW Menke's disease; nerve damage; trauma; ischaemia; stroke; ss.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT 1..2985  
 FT /\*tag- a  
 FT s1g\_peptide 1..78  
 FT /\*tag- b  
 FT mat\_peptide 79..2982  
 FT /\*tag- c  
 XX M09714966-A1.  
 XX 24-APR-1997.  
 XX 10-OCT-1996: 96WC-CA00679.  
 XX 13-OCT-1995: 95US-0005518.  
 XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 XX Henkemeyer M, Pawson A;  
 XX MPI: 1997-245245/22.  
 XX P-PSDB: AAW26366.  
 DR Activation of ligand regulatory pathways by Eph subfamily receptor  
 PT tyrosine kinases - for stimulating or inhibiting axonogenesis,  
 PT useful for treatment of e.g. neurodegenerative diseases such as  
 PT Alzheimer's or Parkinson's diseases  
 PS Disclosure: Page 24-25: 55pp; English.  
 XX This cDNA sequence codes for murine Nuk tyrosine kinase (AAW26366),  
 CC an Eph subfamily receptor tyrosine kinase essential for formation  
 CC of the medial tract of the anterior commissure of the brain. Its  
 CC sequence was deduced from clones isolated from an embryo cDNA  
 CC library in lambda gt10. The Nuk gene maps to the distal end of  
 CC chromosome 4 near the abd-1 mutation. Eph subfamily receptor  
 CC tyrosine kinases (e.g. Nuk extracellular domain polypeptides)  
 CC can be used in claimed methods to: activate a ligand regulatory  
 CC pathway in a cell; identify a substance able to bind a ligand for  
 CC an Eph subfamily receptor tyrosine kinase; and to affect neuronal  
 CC development or regeneration, especially the stimulation or  
 CC inhibition of axonogenesis, in a mammal. Activation of the ligand  
 CC regulatory pathway results in downstream activation of a series of  
 CC regulatory pathways in cells that control gene expression, cell  
 CC division, cytoskeletal architecture, cell metabolism, cell  
 CC migration and cell-cell interactions. Substances which activate  
 CC the ligand regulatory pathway may be used for stimulating or  
 CC inhibiting neuronal development regeneration and axonal migration  
 CC associated with neurodegenerative disease e.g. Alzheimer's,  
 CC Parkinson's or Huntington's diseases, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, deficiency diseases such as  
 CC Menke's disease, peripheral nerve damage, trauma and ischaemia  
 CC resulting from stroke.  
 XX Sequence 3105 BP; 710 A; 937 C; 848 G; 610 T; 0 other;

Db 127 tgaatgtatcccccacacgaaggtggaaggtgagcggtacagacgaatcgaac 186  
 QY 121 ACGATCCGACAGCTACCAAGTGTGTGAACGTGTGTGACGAAGCAACTGGCTACGG 180  
 Db 187 actaccgtacacacacaggtgtgcaatgtcttgaagcaagcgaacaaactgtcgtcg 246  
 QY 181 ACCAAGTTTATCCGCGCCGCTGGGGCCACCAGCATCCACGCTGGAGATGATGTTTGGTG 240  
 Db 247 accaaatcaccgcgcgtgtggtcccaacgataccagctggaagatcgaagtcgtcg 306  
 QY 241 CGTACCTGCAGACGACATCCCAAGCGTCCGTGCTGTGCAAGAGACCTTCAACTGTAT 300  
 Db 307 cgtgacgtcagcagcatctcccaagcgtgtccggtctccgtcaagagacatccacatc 366  
 QY 301 TACTATGAGCGCTGACTTGTGACTGGCCACCAAGACTTCCCAACAGTGAATGGAATCCA 360  
 Db 367 tactatgagcgtgattttgtacttagcacaacaaactctcccaactggaatggaatccg 426  
 QY 361 TGGGTGAAGGTGATACCATTTGACGCGACGAGAGAGCTTCCCAAGGTGACCTGGGTGCG 420  
 Db 427 tgggtgaaggtgagacacacacacgcgcgtgagagcttctcgaagtgagccgtgtgagc 486  
 QY 421 CGGCTCATGAAATCAACACCGAGGTGCGAGCTTGCGAGCTGTGTCCGACGCGCTTC 480  
 Db 487 cggctcatgaaatcaaacacacacacacacacacacacacacacacacacacacacac 546  
 QY 481 TACCTGCGCTTCCAGAGACTATGCGCGCTGATGCCCTCATGCCGCTGCTCTAC 540  
 Db 547 tacttgcccttccaggaactcgcgcgtgtgtatctccatctgtgtgtgtgtgtgtgtgt 606  
 QY 541 CGCAAGTGGCCCCCGCATTCAGAAATGGCGCATCTTCCAGGAACCTGTGCGGGCTG 600  
 Db 607 cggaaagtgtcccccgaaatcaacacacacacacacacacacacacacacacacacac 666  
 QY 601 GAGAGACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 Db 667 gagaagacatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 726  
 QY 661 GTACCCATCAAGCTCTACTGTATACGGGAGCGGAGCTGTGTGCTGCTGCTGCTGCTGCT 720  
 Db 727 gtgcccatacaactctacacacacacacacacacacacacacacacacacacacacac 786  
 QY 721 ATGTGCAAGCAAGCTTTCGAGCGCTTGAAGATGCAACGCTGTGCGGAGCTGTGCTCAT 780  
 Db 787 atgtgcaagcagcgtctcagagctgtggaagcagcgtctcagagctgtgtgtgtgtgt 846  
 QY 781 GGGACTTTCAGGCGCAACCAAGGAGTGAAGCTGTGACCATGCTTCCATCAACACCGCG 840  
 Db 847 ggaacttcaagcgcaacaaagggagagacgtgcaacacacacacacacacacacacac 906  
 QY 841 ACCACTTCTGAAGGGGCAACAACCTGTGTGCGCGAATGCTACTACAGACAGACTGTG 900  
 Db 907 accaactctgaaggggtgtcccaacacacacacacacacacacacacacacacacacac 966  
 QY 901 GACCCCTTGACATGCTTCCGACACACATCCCTCGCGCCCGCAAGCTGTGATTTCCACT 960  
 Db 967 gaccccttgaatgtcttgcacaaacacacacacacacacacacacacacacacacac 1026  
 QY 961 GTCAATGAGACCTCCCTCATGCTGAGTGGAGACCCCTCCCGGAGCTCCGAGAGCGAGAG 1020  
 Db 1027 gtcaaatgagacctccctcatgctgagtgagtgagtgagtgagtgagtgagtgagtgag 1086  
 QY 1021 GACCTGCTTACACATCATCTGTGCAAGAGCTGTGCTGCGCGGGGCTGTGACCCGC 1080  
 Db 1087 gatctgtttacaacacacacacacacacacacacacacacacacacacacacacacac 1146  
 QY 1081 TGGGGGAGACAATGTACAGTACGACACCAAGCTGACCTTACACGACGACGACTTTAC 1140  
 Db 1147 tgggggagacaatgtacagtagacacacacacacacacacacacacacacacacacac 1206  
 QY 1141 ATCAAGTACCTGCTGCGCCACCAAGCTTACACTTCCGAGATCCAGGCTGTGACCGGCTT 1200  
 Db 1207 atcagtgacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1266





OY	1615	CTCATTCCTGTGGTTGTCATCGCCATCGTGTGTAACACACGGGGGTTTGAOCGTGCTGAC	1674
Db	1687	ctctccgtcttggtctgcattcccatcgtatgtatcaacaaggggttgtagtcgtccgac	1746
OY	1675	TCGAGATACACGGACAAGCTGCAACACTACACCACTGTGGCCACATTAACCCAGGATCAAG	1734
Db	1747	tcgaagtaccacggaacaagtctacagacactaccacagcggacaacatagaccccaagatgaag	1806
OY	1735	ATCTACATCGATCCCTTTACCTACACGAGGACCCCAACGAGCATGTGCGGGATTGTGCCAAG	1794
Db	1807	atcctatagatccttccctacccctctagtaagcttcctaaatgtagcagtgctggaattgtccaaag	1866
OY	1795	GAATTAATCACTTCCTGTGTCAAAATTTGAGCGAGGTGATCGGACGAGGGGAGATTGTGGCGAG	1854
Db	1867	gaaatgtacacctccctcgtgtccaagaattgcagcagcgtgtgtgagcaagggaaattgtgtgag	1926
OY	1855	GTCGTGCAGTGGCCACCGAAGCTGCCAGGACCAAGAGAGATCTTGTGTGGCCATCAAGACG	1914
Db	1927	gtctcgaagtgccaatttgtaagctgtgcgaagcagaagagatcttgttagcatcaagacc	1986
OY	1915	CTCAAGTCGGGCTTACACGGGAAGCAGCGCCGGGACTTCCTAGAGGAGCCTTCATCATG	1974
Db	1987	ctcaagtgcaagatacaagtgagaaacagcgcggtgactcttcgaatgagagctccatcagt	2046
OY	1975	GGCGATTTCGACATCTCCCAACGTATACCTCAACCTGTGAGGGGTGTGTGACCAAGACACACT	2034
Db	2047	ggccaggttcgaccccccaatgtcatccatctcgtgaagggtgtgtacccaagacacacct	2106
OY	2035	GTATGATCATACCCAGGTTCAATGAGAGAAATGGCTCCCTCGCATCTCTTCTCCGGCAAAAC	2094
Db	2107	gtcatgtacatcaacttgaattcatcctagagaatgtgctctcgtgactctctccctccggaaaat	2166
OY	2095	GATGGGGAGTTCACACAGTATCCACGCTGTGAGGGGATGCTTTCGGGGGATCGCACGTGGCATG	2154
Db	2167	gattgggcagttccacagatccatccacactcgtgtggtgagatgtctgaagggttatgtcaagccgagc	2226
OY	2155	AAATGACTGGCAGACATGAACATATGTTCAACCCGTGACCTTGCTGGCCCGCAACATCCTGTGC	2214
Db	2227	aagtaacctggtgagacatgaactactgtgcacgcgtgacctgtcgtcgtcgaataactctcgtc	2286
OY	2215	AACACGACCTGAGTCTCCAGAGGTGTGGGACTTTTGGGCTCTACGCGTTTCTATGAGAGCAGAT	2274
Db	2287	aacagtaacctgtgtgtatgaagtgtctgactgtacttgggtctctcaagcttccctgtgaagatgac	2346
OY	2275	ACCTCAGACCCCACTACACCACTGCCCCCTTGCGGCGAAAGTTTCCCATTCGCTGCAACGCC	2334
Db	2347	acgtctgaccccaactctacaaagcgtctctgtgtggaagaatccatccatctgtgtgagcgtca	2406
OY	2335	CCGGAAGCATTCACGATCCGGAAGTTCACTCCGCGACGATGTGTGAGGATCGATACGCGATT	2394
Db	2407	ccggaagcaccatccagtaaccggaataatcaacctcgtgcagatgtagtgtggaagctatgtgtac	2466
OY	2395	GTCATGTGGGAGGTATGTCTCTATGAGGGAGCGGCCCTACTGTGGACATGACCAACCAAGAT	2454
Db	2467	gtcatgtgtgaggtgtgtagtctctactacggaagacccctactgtgagacatgaccaataagac	2526
OY	2455	GTAATCAATGCCATTGAGCAGAGACTATTCGCGCTGCAACGCCCATGAGACTGCCCCGAGCGCC	2514
Db	2527	gtaatccaagccatctgaacaggaatlaagaactctctccgccaatgaaatgtcccttagtcgc	2586
OY	2515	GTCGACCAACTCATGCTGTGAGCTGTGTGGCAAAAGACCGCAACCAACGCGCCCAAGTTTCGC	2574
Db	2587	ctgcaccacgctcatgtctgtagctgtgtgcagaagagacccaacccggtcccaagttgcgc	2646
OY	2575	CAAAATGTCAACAGCGTATGACAGAGATGATCCGAATTCCTCAACAGCTCAAAACCATGGCG	2634
Db	2647	cagattgtccaacaagctgtgaaagaatgatctcggaaaccccaagcctccaagaactgtgca	2706
OY	2635	CCCGCTCTCTCGGATGATCAACTGTCGCGCTGTGTGACGACGACGATCTCCCGCATACACAGC	2694
Db	2707	ccccgttccctcgtgataccaacctgcacgtcgtgtgaacgcgcagatctacgcgaactaacccagc	2766
OY	2695	TTTAAACAGGTGTGACGAGTGGCTGTGAGAGCCATCAAGTGGGGCATTAAGAAGAGACTTTC	2754

[illegible]

## RESULT 7

AAQ90660  
ID AAQ90660 standard; DNA; 4049 BP.

AA  
AC AAQ90660;

DT 11-NOV-1995 (first entry)

DE Eph-related PTK Cck5.

AA Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
 KW Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

KW prognosis; ss

OS Gallus sp.

.....	Key	Location/Qualifiers
FH		

FT	CDS	1
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XX

XX 3 PM 100E

XX 02 SEP 1994 0440-7610140

XX 03 FEB 1963 0345C-0163800

XX  
XX  
(101- ) IN TOTAL CANTER RES FOUND

XX  
XX

XX  
XX  
WPT. 1005-315356/38

DR P-PSDB; AAR75712.

PT Eph-related prote

XX  
Page 93-96: 129nn: English  
Description:

XX probes derived from the FPH-related PTGs Cex4 (AA090659) and Cex5

CC (AAQ90660) were used to isolate novel  
CC (AAQ90661-62) from chicken embryo and embryonic brain libraries.

Sequence 4049 BP: 1010 A: 1011 C: 1072 G: 956 T: 0 other:

Query Match	Score	DB ID	Length
Best Match	73.8%	2187.2	4055
Best Local Similarity	84.1%	Pred. No. 0	

Matches	2494;	Conservative	0;	Mismatches	405;	Indels	5;	gaps	2
---------	-------	--------------	----	------------	------	--------	----	------	---

oy 1 CTGCTCGCCGGCCTGGAGAAACGCTAATGGACTTCACIACACCGACICGCGAGCAGCCC

Dd 76 ctgctcgcgcccgatggaaagacgcacgaaccccaaacgccccagccccccc

61 TGGATGTCATCTCTCATCAGGGTGGAGAGGTGAAGTGGCTTACGATGAGAACTGAAAC 120  
136 Tggagtggtgcatctctccctccaggtgaggaagtgagtgagataagatgagaacatgaaac 195  
121 AGGATCCCGACAGTACGAGTGTGCAACGTGTTGATGCAAGCCGAGAACTGGCTACGG 180  
196 accatccgacatccacagatgtgcaagctcttgaaatccacccaataaactggtcgtcg 255  
181 ACCAAGTTTATCCGGCCGCGGTGGGGCCACCGCATCCAGTGGAGATGAAGTTTTCGGT 240  
256 accaagatcatccggaagcgagagcgacatccacgfygagatgaaatcttcgct 315  
241 GGTGACTGACAGCATGATCCCAAGGCTGCTGCTCTGCAAGAGAACCTTCAACCTTAT 300  
316 cggagctgcaagacatcccaacgctcccggtctctgtlaaggagaaacttlaacctctat 375  
301 TACTATGAGGCTGATTTGATGACTCGGACCAAGACCTTCCCAATGGATGGAGATTCGA 360  
376 tactaagaaatcagacttgacttgctgcacccaagacttctctaactggaatggaataacct 435  
361 TGGTGAAAGTGTGATPACCATTTGCAAGCCGACGAGATTTCTCCAGTGGACCTGGTGGC 420  
436 tggatgaaagtatgaataacacggaagtgccgacgtctctcgacgttgagacctgtgtcg 495  
421 CGCGTCAATGAATAACACCGAGGTGGGAGCTTCCGAGCTGTGTCCCGACGCGCTTC 480  
496 cgggtgatgaaatlaaacaacggaagtgccgagtttgagccttctcctcaaaaacgcttc 555  
481 TACCTGGCTTCAGAGATATGGCGGTGATGCTTCCTCATCGCGCTGCGGCTTCTTAC 540  
556 tactctgcctcccaagactaagcggtgtgcaatgctccttgatgtgagtcggtctcttacc 615  
541 CGCAAGTGGCCCCCATCATCTCAGAAATGGCGCATCTTCCAGAAACCTGTGCGGGCT 600  
616 cgaagatgctcccgctgtaaccagaacggtggtctctccaagaaacctctcgagcg 675  
601 GAGAGCATATGCTGTGGTGGTCCCGGGGAGCTGATCCCAATGGGGAAGAGTGGAT 660  
676 gagagacatctctgtgtgcaagccgggggagcgtgcatcgaatgagagaggtgtgat 735  
661 GTACCCATCAAGCTCTACTGTAAAGGGGAGGAGGAGTGGTGGTCCCATCGGCGCTGC 720  
736 gtgcacatcaagctgtactgtaactgtggatgtgagatgtgtgtgtcccatcggtcgtgc 795  
721 ATGTGCAAAACAGGCTTCGAGGCGTTGAGAAATGGACCGTCTGCCGAGTTTGCATCT 780  
796 atgtgcagcgccgggtctatgagtcgtgtgagaaatggacgtctgcaagagctgtcccatca 855  
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856 gggaaacctcaaggtccagccaaggaatgaaatgtgtgtcattgtccaattaaacagccgg 915  
841 ACCACTTTCGAAGGGGCGACCAACTGTGTCTGCCGAATGGTACTACAGAGAGACCTTG 900  
916 acgaacttcgaaagggccaaagactgtgtgtgcgaagaaatatacccggtgaagtgtct 975  
901 GACCCCTGGACATGGCCCTGCAACACATCCCTCCGCGCCCAAGGCTGTGATTTCCACT 960  
976 gaccccgctgcaatgtgcaatgacacacatcccaatctgtcccccagagccgtgtactccagc 1035  
961 GTCAATGAGACCTCCCTCATGCTGAGTGAACCCCTCCCGGAGACTCGGAGGCGGAGAG 1020  
1036 gtgaaatgaaacctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1095  
1021 GACCTGCTACACAACTATCTGCAAGAGCTGTGCTCGGGCGGGGCTCTCTACACCCG 1080  
1096 gactctgtatatacaatactatctgcaagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1155  
1081 TGGGGGAGCAATGTACAGACGACACGCGCAAGCTAGGCTTACGAGACGACGACATTTAC 1140  
1156 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1215

1141 ATCAGTACCTGCTGTGGCCACACCCAGTACACCTTCGATGCCAGGCTGTGAAGGGGCTT 1200  
1216 atcaaggaactcgtcgtggcccaacagatlaacactcttgatgtatcaagctgtgtgtgtgt 1275  
1201 ACTGACCAAGGCCCTTCTCGGCTCAAGTTGCGCTGTGTGAACATCAACCAACCAAGCA 1260  
1276 accgaaccagagccctctctcccccagcttgcatacagtgaaatataccaccaacagagct 1335  
1261 GCTCATCGGAGTGTGCATCATGATGATGAGCGGACCCGTCAGTGGACGATTTACCTTG 1320  
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1321 TGTGTGCCAGCGGAGCAAGCCCAATGGCGTATCCTGTGATCATAGAGTGTGATGAT 1380  
1396 tctgtgtcaacctgacagcccaatggtgtatctctgtatataatgagctgtgcaatactat 1455  
1381 GAGAAGAGCTCAGTGAAGTCAACGCCACAGCCATTAATAAAGCCCAACCAACGCTTACG 1440  
1456 gagaagaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1515  
1441 G-----GCTCAAGGCGGCGCCATCTATGCTTCCAGGTGGGGCAGCGACTGTGGCA 1494  
1516 gtgcaaaacctcaagctgtgcaacacatctatgtctctcaagtgagacagctacacgtgtgt 1575  
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1615 CTCTATGCTGTGCTGTCTCATCGCCATCGTGTGTAAAC---AGACGGGGGTTTGGGCTGTG 1671  
1696 ctctatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1755  
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1756 gactctgtatcatctgtacaagctgtgacactataccagtggtgtgtgtgtgtgtgtgtgt 1815  
1732 AAGATCATATGATGATCTTCACTTCACTGAGAGACCCCAACGAGGAGTGGGGAATTTGCC 1791  
1816 aagatctatcatcatcatctatctcaagaaatcccaatgaaagctgtgtgtgtgtgtgtgt 1875  
1792 AAGGAATTTGACATCTCCGTGTCAAAATTTGAGCAGGTGATGGAGAGGGAGTTTGGC 1851  
1876 aaagaatctatcatctccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1935  
1852 GAGTCTGCAAGTGGCCACTGTAAGCTGCCAGGCAAGAGAGATCTTGTGGCCATCAAG 1911  
1936 gagtgtgtgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1995  
1912 ACGCTCAAGTGGGGCTAACCGGAGAAAGCAAGCGCCCGGACTTCTTGAAGGAGACCTTCATC 1971  
1996 acccgaaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2055  
1972 ATGGGCAATTTGACCATCCCAACTCATTCACCTGTGAGAGGCTGTGTGACCAAGAGACA 2031  
2056 atggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2115  
2032 CCTGTGATGATATATACCGAGTTTCAATGAGAAATGGCTCTCTGTGAGCTCTTCTCGGCA 2091  
2116 ccagttcatatcatatcatatcatatcatatcatatcatatcatatcatatcatatcatat 2175  
2092 AACGATGGGAGTGTACAGTATCCAGTGTGAGTGGGCAAGTGTGGGAGATGGAGCTGTGGC 2151  
2176 aatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2235  
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2236 atgaagtacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2295  
2212 GTCAACGACAACTGTGTGTGCAAGTGTGTGACATTTTGGGCTCTCAAGCTTTCTGTAGAGAC 2271



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Db      2296  gtcaacagcaaccctgctcgaaggtgctcgaactgcgcctctccctgctcctggaagat 2355
OY      2272  GATACCTCAGACCCCACTACACAGTGCCTGGGCGGAAGTCCCATCGCTGGACA 2331
Db      2356  gacacctctgacccaactacacagcagcagctggtggaagaatcccaatcggctggaca 2415
OY      2332  GCGCCGGAAGCCATCCAGTACCGGAAGTTACCTCGGCCAGTGTGTGAGTACCGC 2391
Db      2416  gcgcctggagcaatcagctacggaataatcacaatcagcagcagctggtggaagatgga 2475
OY      2392  ATTGTCAATGTGGAGAGTATGTCTCATGGGAGGCGCCCTACTGAGACATACCAACAG 2451
Db      2476  atagctatgtggaagtgatgctgacgagcgagccttactggaacatgacacatcaa 2535
OY      2452  GATGAATCAATGCAATGAGCAGAGTATGAGTATGCGTCCAGCCCGCATGAGTACCGCAGC 2511
Db      2536  gatgtgataaatgctatctgagcagagctatcgctacacacccctatgattgtccaat 2595
OY      2512  GCCCTGACCAACTCATGCTGAGTCTGTTGGCAGAGAAGACCGACACCGCCCAAGTTC 2571
Db      2596  gccctgcacacgaactaactgtcagctgctgagaaagatcgaaacacagaccccaattt 2655
OY      2572  GGCCAAATTTGACACAGCTAGACAAGATGATCCGCAATCCCAACAGCCTCAAGCATG 2631
Db      2656  ggcagatgtgcaacacttagacaataatgacgaataatcctaataatgactgaaagcatt 2715
OY      2632  GCGCCCTCTCTCTCTGCGATCACTGCGCTGCTGAGCAGCAGCATCCCGCATACACC 2691
Db      2716  gaactctctctctctggtggttaactcctcctactgacacacacacacacattatacc 2775
OY      2692  ACCTTTACACGCTGAGAGAGTGGTGGAGGCGCATCAAGATGGGAGTACAAGAGAGAC 2751
Db      2776  agcttcaaacacgtggaatgaaatgctgagctgcaatcaagaatgagcagtaagaagagc 2835
OY      2752  TTGCGCAATGCCGGCTTCACTCTCTTGAAGTCTGTCTCAGATGATGATGAGAGACAT 2811
Db      2836  ttgccaagctgctggtctcaacacacttgatatactcagatgacgtgtagaagacatt 2895
OY      2812  CTCGCGGTTGGGCTCACTTGGCTGGCCACGAGAAAAAATCCTGAACGATGCCAGGTG 2871
Db      2896  ctacagctggtggtacattttagacagacacagaaagaaatcttgaacagatccaggtg 2955
OY      2872  ATGCGGCGCAGATGAACAGATTCAGTCTGTGAGAGTTTGACATTCACCTCGCGCT 2931
Db      2956  atgagagacacagatgaacaaatcagctgtggtggtttgtagaacaacagctccgtg 3015
OY      2932  CACCTCTCTCTCAAGCCCGCCGCC 2957
Db      3016  ctccactctcttgagcgccctgctccc 3041

RESULT 8
AAQ90657
ID      AAQ90657 standard; DNA; 4097 BP.
XX
AC      AAQ90657;
XX
DT      11-NOV-1995 (first entry)
XX
DE      Eph-related PTK Cdk5+.
XX
KW      Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
XX      prognosis; ss.
XX
OS      Gallus sp.
XX
FH      Key Location/Qualifiers
FT      10..3045
FT      CDS /tag= a
XX
PN      MO9515375-A.
XX

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PD      08-JUN-1995.
XX
XX      07-SEP-1994; 94MO-US10140.
XX
XX      03-DEC-1993; 93US-0162809.
XX
XX      (JOL-) LA JOLLA CANCER RES FOUND.
XX
XX      Pasquale EB, Sajjadi FG;
XX
XX      WPI; 1995-215256/28.
XX
XX      P-PSDB; AAR75709.
XX
XX      Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
XX      cancer.
XX
XX      Claim 2; Page 71-75; 129pp; English.
XX
XX      A cDNA clone encoding a novel variant of Eph-related PTK Cdk5,
XX      Cdk5+ (AAQ90657), was isolated from a chick embryo library in
XX      lambda gt11. Cdk5+ protein (AAR75709) contains a 16-amino acid
XX      insertion in the juxtamembrane domain, and be a result of
XX      alternative splicing. Cdk5+ is exclusively expressed in the CNS.
XX
XX      Sequence 4097 BP; 1014 A; 1029 C; 1087 G; 967 T; 0 other;
XX
Query Match 71.8%; Score 2127.6; DB 16; Length 4097;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 464; Indels 57; Gaps 3;

OY      1 CTGCTCGCGCGGTGAGAAAGCCTAATGAGTCTCAGTACGAGTCTGAGACTGGC 60
Db      76 ctgctcgcgcgcgtggaagagcgtgagtgactccacaagcagcagcagcgtggtgc 135
OY      61 TGGATGTGATCCTCCATTCAGGGTGGAGAGGAGTGGCTGATGAGATGATGAAC 120
Db      136 tggatgtgcatcctccatctcaggggtggaagagtgagtgatgatacgtggaacatgaac 195
OY      121 ACGATCCCGAGTACAGAGTGTGCAACGTGTTGATGCAAGCCAGAACACTGCTACCG 180
Db      136 tggatgtgcatcctccatctcaggggtggaagagtgagtgatgatacgtggaacatgaac 195
OY      196 accatccgacactacacagtggtgcaagctcttgatccagcacaacaaactgctgcg 255
Db      121 ACGATCCCGAGTACAGAGTGTGCAACGTGTTGATGCAAGCCAGAACACTGCTACCG 180
OY      181 ACCAAGTTATCCGCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGATTTGGTG 240
Db      196 accatccgacactacacagtggtgcaagctcttgatccagcacaacaaactgctgcg 255
OY      256 accaagttatccgcgcggtggggtggggtggggtggggtggggtggggtggggtggg 315
Db      241 CGTGAAGTATCCGCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGATTTGGTG 240
OY      316 cgtgactgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 375
Db      301 TACTATGAGGCTGACTTGTGACTGGCCACAGACCTTCCCACTGATGAGATGCA 360
OY      376 tactacgaatcagacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 435
Db      361 TGGGTGAAGTGAATACATTCAGCTGACCGAGAGCTTCTCCAGATGAGATGAGTGGC 420
OY      436 tggatgaagtgatgaatcatttgcgcagcagcagcagcagcagcagcagcagcagc 495
Db      421 CGCGTATGAATAATCAACACGAGGTGGGAGCTTGGAGACTGTGTCCGCGAGCGGCTC 480
OY      496 cgggtgatagaatataacacagcagcagcagcagcagcagcagcagcagcagcagc 555
Db      481 TACCTGGCTTCCAGTATGAGCGCTGATGCTCCATTCATGCGCGTGTCTTTCAC 540
OY      556 tacttgccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 615
Db      541 CGCAATGCGCCCGCGCATATCCAGATGAGCGCATCTTCAGAGAAACCTGTGCGGGGCT 600
OY      616 cgaagtgctcccggtggtgacgaagcagcagcagcagcagcagcagcagcagcagc 675
Db      601 GAGAGCACATCGCTGTGCTGCTCCGCGGCGAGCTGATGCCAATGCGAGAGGTGAT 660

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Db 676 gaaagacaatctctgctgagccggggagacgtgcatacgaatcgcggaagctgcat 735  
Oy 661 gTACCATCAACCTTACTGTATGAACGGGAGCGGAGTGGCTGGTGGCCATCGGGGCTGC 720  
Db 736 gtgcccaataagctgtactgcaatgagatgagctgagctgagctgagccatcgccgcgcg 795  
Oy 721 ATGTCAAAAGCGGTTTGAGGCGCCTTGAAGATGGACACCGTGTGCCGAGGTTGTCCATCT 780  
Db 736 atgtcaaaagccgggtctatgaatcgtgtgagaaatgagaccgtctgcgaagcgcgcacatca 855  
Oy 781 GGGACTTTCAAAGGCGCAACCAAGGCTGAGGCGCTTACCCACTGTGCCATCAACAGCGGG 840  
Db 856 gggacccttcaagggccagcagaagagaaatgaagaaatgctccatctgtccaaatlaaagccgg 915  
Oy 841 ACCACTTGTGAAGGGGCGCACCAACTGTGTCTGCCCAATGGCTTACTACAGACAGACCTGG 900  
Db 916 agactctgaaagggccagaaatcgcgtgtgcgaaacggaatatataccgagcagaatgct 975  
Oy 901 GACCCCGTGAATGCTTCCCTGCAACCAATCCCTCCGCGCCCGAGGCTGTGATTTCCAGT 960  
Db 976 gaccctcgtaagaaatgcaatgcaacacacacacacacacacacacacacacacacacacac 1035  
Oy 961 GTCAATGAGACCTCCCTCATGCTGAGTGGAGGAGACCCCTCCCGGACCTCCGGAGCGGAGAG 1020  
Db 1036 gtgaatgaataacctccctgtaatgctgagatggaaccccaacacagaaactcagaagccgag 1095  
Oy 1021 GACCTCGTCAACATCATGTGCAAGAGCTGTGGCTCGGGCCGGGGTCCCTGCACCCGC 1080  
Db 1096 gatctgtatatacaatcatcatctgcaagacgtgtggtcagacgctlggggcgtgcaacgag 1155  
Oy 1081 TGGGGGACATGTATAGTACGACACACGACGATAGGCGCTGACCGACCGCATTTTAC 1140  
Db 1156 tgtggggaacaaatgcaatcttgcacccagcagcagcagcagcagcagcagcagcagcagcag 1215  
Oy 1141 ATCAGTGAACCTGTGGCGCACACACAGTACACTTTCGAGATCAGGCTGTGAACGGCGCTT 1200  
Db 1216 atcagcgaaacctgctgcccacaagacagaaaccttgaagataccagcgtgtgaatggygctc 1275  
Oy 1201 ACTACACGAGACCCCTTCTGCGCTCAAGTTCGCTGTGAACATACCAACCAACGAGCA 1260  
Db 1276 accgaacgaagccctctctccacacacacacacacacacacacacacacacacacacacac 1335  
Oy 1261 GCTCATTCGCGAGTGTGCATCATGATCAGTGTAGCGCGGAGCGGACAGCATTAACCTTG 1320  
Db 1336 gtctcttcagcgcgtgtccataatgcaacagatcagccgacatcgtgcaagaataatcaacctc 1395  
Oy 1321 TCGTGTGCCAGCGCGGACCAACCCCAATGGCTGTGACTGTGAGCTGTGAGCTGACTACTAT 1380  
Db 1396 tctgtgtctcaacctgaacgaaccccaatgagatcactctgtgataatgagctgcaatactatc 1455  
Oy 1381 GAGAAAGAGCTCATGTAGTACACGCCACAGCCATTAAGCCCAACCAACAGGCTACG 1440  
Db 1456 gagaagaacatcgtgagcttaataatcacaacagcagtgaaagccccaacacacacacacacac 1515  
Oy 1441 G-----GCCCTAAAGCCGCGGCATCTATGTCTTCCAGGAGCGGGACAGCATGTGGCA 1494  
Db 1516 gtgcaaaaacctcaaaagctgtgcacacatctatgtctctccaagtgtgagcaatcagctgagct 1575  
Oy 1495 GGGTACGGGCGCTTACAGCGGCAAGATGTACTTCCAGACCATGACAGAGCGGAGTACAG 1554  
Db 1576 gggtaatggtccggtatagctgcaagaatgtacttccagaacacatgaaatgaaagccgagtaaccag 1635  
Oy 1555 ACAAGATTCAGAGGAGGAGTGGCCATCATGATGGCTCCCGCGCGCTGGCGCTGTTC 1614  
Db 1636 accagatctcagaagaagacgtgcacacatcaltgtgcccctcctcagaagaatcgtgtctt 1695  
Oy 1615 CTGATTCGTGTGTGTTCATCGCATCGCATGTGTGAAC---AGAGGGGGGTTTGAAGCGTCT 1671  
Db 1696 ctcatctgtctgtgtcgtcatcatatctgtctgcaaaagaagaagggccttgaagcgtct 1755  
Oy 1672 GACTCGGAGTACAGGAGCAAGCTGTCAACACTACACAGTGTGCCACA----- 1717  
Db 1756 gaactctgatacactcgtcaagaagctgcaagactataacagtggtccaaagtaagtaacgtgct 1815

Oy 1718 -----TAAACCCAGGATGAAGATGTACATC 1743  
Db 1816 cccccgcaagcccggtggtccgtctctctctctctgtgtactccagaagaaatctatactc 1875  
Oy 1744 GATCCTTTACCTTACGAGAGACCCCAACGAGCAGTGGCGGAGTTTGGCAAGAAATTGAC 1803  
Db 1876 gatccatttacctgaagaatcccaatgaaatgagctgtcgaaggaaatctgcaaaagaatctgat 1935  
Oy 1804 ATTCCTGTGTCAAAATTTGACAGAGTGTATCCGAGCAGGGGAGTTTGGCAGGCTGTGCACT 1863  
Db 1936 atctcgtgtgtaaaatcgaacagtgatctgtggcagaaggagcttggatgaaagtgctgagct 1995  
Oy 1864 GGCACCTGAAGCTGCCAGGAGAGAGATGATCTTTGGCGCATCAACAGCCTCAAGTCG 1923  
Db 1996 ggtgcatctcaagcttctctgcaaaaagaagaatctctgtgccaacaaacccatgaagctc 2055  
Oy 1924 GGTACACGGAAGACAGCGCGGAGCTTCTGTAGCGAAGCCTTCATCATAGGCGCAGTTTC 1983  
Db 2056 ggtacaagaagaagcagaagacggaacttctgtgagtgaaagccatcatatgagggcagctt 2115  
Oy 1984 GACCATCCCAACGTCATCCACTTGAGAGGTGCTGTGACCAAGACACACCTGTGATGATC 2043  
Db 2116 gaccaccccaatgtcatccacttgaaaggggtgtgtgaacaaagatctcccaatcatatgac 2175  
Oy 2044 ATCAACGAGTTTCATGAGAAATGGCTCCCTGGACTCTTTCGCGCAAAAGATGGGCGAG 2103  
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Oy 2104 TTTCAGACTTCACAGCTGTGTGGGCGATGCTTTCGGGGCATTCGACGTGGCATGAAGTACCTG 2163  
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Db 2296 gctgataatgaactcaatgcaacagagacgtgctgcccgaacacacccgtgtcaaaagaac 2355  
Oy 2224 CTGGTGTGCAAGGTGTGGGAGCTTTGGGCTGTCAAGCTTTTGTAGAGAGATTAACCTGACAG 2283  
Db 2356 ctgtctcgaaggtgtcgtgactctgcgtctccgcttctctgtgaaggtgtgcaactctgat 2415  
Oy 2284 CCCACCTACACACAGTGGCCTGTGGGCGGAAAGTTCCCACTCCGCTGTGACAGCCCGGAGCC 2343  
Db 2416 ccaacttacaacccagcagcagctgtgaaagatcccaatlaagtgagacagcgtgagca 2475  
Oy 2344 ATCCAGTACCGGAAGTTCACCTCGCCAGATGATGTGTGAGCTACGGCATTTGCATGTGG 2403  
Db 2476 attcagtaaccgaaatctacatacagccagcgaatgtgtgagcctatgaaatagatcaatgtg 2535  
Oy 2404 GAGGTATGTCTATGTGGGAGCGGCCCTACTGTGGACATGACCAACAGATGTAATCAAT 2463  
Db 2536 gaagtgtgtctgtacagcgtgagcccttactgtgaaatgacatgaatgctgataaat 2595  
Oy 2464 GCCATTGAGCAGACTTTCGGGCTGCCACCGCCCATGTGACTGTGCCGAGCGCCCTGCACCA 2523  
Db 2596 gctatgtgaagaagacatctggtctacaaaccccaatgagatgtgtcaaaatgctgcacccag 2655  
Oy 2524 CTGATGTGAGCTGTGGGAGGAGCAGCAGCAACCGGCGCAAGTTTGGCCAAATTTGTC 2583  
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Oy 2584 AACACGTTAGACAAAGATGATCCCAATCCCAACAGCCTCAAAAGCCATGCGCCCTCTCC 2643  
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Oy 2644 TCTGGCATCAACCTGCGCGCTGTGGAGCAGCAGATCCCGCACTACACAGCTTAAACAG 2703  
Db 2776 tctgaggttaacctctctctactgtacgtgcaaaatcccaagataatcaacagcttcaaacact 2835  
Oy 2704 GTGACGAGTGTGTGAGGCGCATCAAGATGTGGGAGTACAGAGAGAGCTTCCGCAATGCC 2763  
Db 2836 gtgatagaatgtgtgtgtgtacatcaagaatgagccagtaacaaaggagagcttctgcagctgct 2895

Oy	2764	GGCTTCACCTCCTTTGACGCTGCTGCTCAGAGATGAGAGACATCTCCGGGTGGG	2823
Db	2896		2955
Oy	2824	GTCACCTTTGGCTGGCCACCAGAAAAAATCCTGAACAGATATCCAGGTGATGCGGGCAG	2883
Db	3016	atgaaccacaattcagctctgtgaggtttgatgaacaacgctcctgltccacttcctt	3075
Oy	2884	ATGAACCGAGATTCACTCTGTGGAGGTTTGACATTACCTCGCTCGGCTACCTCTTCTTC	2943
Db	3016	atgaaccacaattcagctctgtgaggtttgatgaacaacgctcctgltccacttcctt	3075
Oy	2944	CAAGCCCGCCCCC	2957
Db	3076	gagggccctgctcc	3089
RESULT 9			
xx	AA053471		
xx	AA053471	standard; cDNA; 4281 BP.	
xx	AA053471;		
Df	16-JUN-1994	(first entry)	
xx	elk cDNA.		
KW	lambda gtl1; expression vector; lambda-BI-Elk; protein tyrosine kinase		
KW	Elk; BI; Eph; subfamily: receptor-like tyrosine kinase; eph; eck;		
KW	phosphorylation; phosphorylated kinase insert domain; growth factor;		
KW	receptor kinase; platelet-derived growth factor receptor; ss.		
xx	Rattus rattus.		
xx	Key	Location/Qualifiers	
Ft	CDS	367..3321	
Ft		/tag= a	
Ft		/product= Elk	
xx	CA2083521-A.		
xx	01-OCT-1993.		
xx	23-NOV-1992;	92CA-2083521.	
xx	31-MAR-1992;	92US-0861390.	
xx	(MOUN ) MOUNT SINAI HOSPITAL CORP.		
xx	Letwin K, Pawson A, Reedijk M;		
xx	WPI; 1993-406300/51.		
DR	P-PSDB; AAR44513.		
PT	Expression of phosphorylated exogenous protein - in host cells		
PT	transformed with two vectors, one for the protein, the other for		
PT	catalytic domain of protein kinase		
xx	Disclosure; Fig 3; 55pp; English.		
xx	This sequence represents the elk cDNA which encodes the protein		
CC	tyrosine kinase, Elk. The Elk gene, BI, encode a protein which is		
CC	a member of the Eph subfamily of protein tyrosine kinases. The Elk		
CC	product is very similar to two other receptor-like tyrosine kinases,		
CC	eph and eck. Lambda-BI-Elk may be used in the production of		
CC	phosphorylated exogenous protein along with a further vector encoding		
CC	the desired exogenous protein. These plasmid may be used to produce		
CC	phosphorylated proteins in host cells which have no intrinsic capacity		
CC	for phosphorylation, eg. bacteria. The system may be used for the		
CC	expression of the phosphorylated kinase insert domain of a growth		
CC	factor receptor kinase eg. platelet-derived growth factor receptor.		
xx	Sequence 4281 BP; 1075 A; 1170 C; 1121 G; 915 T; 0 other;		

Query Match:		55.1%	Score 1631:	DB 14:	Length 4281:
Best Local Similarity		73.0%	Pred. No. 0:		
Matches 2128:		Conservative	0:	Mismatches 780:	Indels 9:
				Gaps	
Oy	5	TCGCGCGCGGTGAAGAAACGCTAATGACCTCCACTTACAGCGACTGCTGAGCTGGGCTGGA	64		
Db	410	tggcgcgatgtagaagaacatctgtagaacaagaagctccacgtcagagatttggatga	469		
Oy	65	TGCTGCATCTCTCCATCAGAGGTGGAAAGGTGAGTGGGTACGATGAGAACTGAACACGA	124		
Db	470	cggcgcaaccctgctcttgggtgggaagatcagtggtcacaagaaaccttgaaccca	529		
Oy	125	TCGCGAGTACACAGTGGTGCACAGTGTGTTGAGTCTCAACCCAGAACACTGGCTACGACCA	184		
Db	590	cccttattacaagaagcggcgccccaatcgcattctatacagaatgcgtcttaacgtgtaggg	649		
Oy	185	AGTTTATCCGGGCGCTGGGGGCCACCCAGATCCTACAGTGGAGATGAAGTTTGGGTGGTGG	244		
Db	245	ACTGCACACACATCCCGACGGTGCCTGGGTCTCTGCAAGAGACCTTCAACCTCTATTACT	304		
Oy	650	actgcagcagccttccaatattgccaggtcctctgtaagaagaccttcaactatactact	709		
Db	305	ATGAGGCTGACTTTGACTGGGCCACCAGACCTTCCCACTGAGTGAAGAAATCCATGGG	364		
Oy	710	atgagactgactctgtcatattgcacacaagaatgcagctctctgtctgtaagcccttaac	769		
Db	365	TGAAGTGGATACCATTTGACGCCGCGAGAGAGGTCTTCCAGGTGGACCTGGGTGGCGCG	424		
Oy	770	tcaagattgacacatattgctgcagatgtagagcttcccaggtgtagatttgggggaaggt	829		
Db	425	TCATGAAATAACAACCCAGAGTGGCGAGCTTGCGACTGTGTGCCGACGCGCTTTTACC	484		
Oy	830	tgtatggaagtcacaacaagaagctcagatcttggcctcttactcagatgtgttllaac	889		
Db	485	TGGCTTCCACAGACTATGGCGGCTGCATGCTCCCTCATGCGCGTGGGTCTTTCACCGCA	544		
Oy	890	tgcgttctccagattatgagacctgtatgtcttactacttctgtccgtgtcttcttcaaaa	949		
Db	545	AGTCCCCCCCATCAATCAACAATGAGCGCCATCTTCAGAGAAACCTGTGCGGGGCTGAGA	604		
Oy	950	agttccacgactgtgtgcaaatatttgcaggtgtccccagaacccaatgcagagacagaga	1009		
Db	605	GCACATGCTGTGTGCTGCCCGGGGCGACGTGCATGCGCATATGCGAAGAAAGTGTGATGAC	664		
Oy	1010	gcaactctctgtgtattgtctcggggacatatgcatctcctaattgcaaaagaattgtagtgc	1069		
Db	665	CCATCAACGCTCTACTGTAAAGGGGAGCGGAGTGGTGGCCATCGGGGCTGTGACTGT	724		
Oy	1070	ccataaactctactgcaatgtagaagatgtagaattgtgacctattgggtgcgtcgcaacct	1129		
Db	725	GCAAAAGAGGCTCTCGAGGCCGTTGAGAAATGGCACCGTGTGCGGAGTGTCCATCTGGGA	784		
Oy	1130	gtaagctcgtgtatgcaac---tgaagaacagctgtgctgcgaagcctgtcctcgtggaa	1186		
Db	785	CTTTCAAGGCCACCAACAGGGGATGAGGCGCTGTAACCACTGTCCTCAACACGCGGACCA	844		
Oy	1187	cccttaaggcagacaggaagctggaagctgcgtcccaatgcgcccccccaacagcgtctccc	1246		
Db	845	CTTTCGAAGGGGCGACCAACTGTGTGTGGCCGCAATGGCTACTACAGACAGACACTGGAC	904		
Oy	1247	cttcaagggcgtctcccaatcgtacccgtgcgagctgtgtattacacgaagacttgaatc	1306		
Db	905	CCCTGAGACGCTTGACAAACCATCTCCCTCGCGGCCCAAGGCTGTGANTTCCATGTCGA	964		
Oy	1307	coccagaagtgtgcgtactagattgtcccaatcgaagcccttgaagaattgcattctcaattgga	1366		
Db	965	ATGAGACCTCTCCCTCATCTGTGAGTGAAGTGAACCCCTCCCGCAGCTCCGAGAGCCGAGAGAC	1024		
Oy	1367	atgaaacatcatatctctgaattgtgcacatctcaagaagaagcgcgttgggcgaagtgtgt	1426		

OY	1025	TCGCTACACATATATCGAAGAGCTGTGCGTCGGGCCGGGGTGCCTGCACCCGCTGC	1084
Db	1427	tgacctacacatacatctcgaaagaatgacagacagaccgagatgtctccgctcgcg	1486
OY	1085	GGGACAAATGTACACTAGCGACCAACGGCAGCTAGCGCTGACGACGACGCAATTTCATCA	1144
Db	1487	atgaaagaatgagatcttgtaaccagaagatgagctctgacatgagtgctgtctataca	1546
OY	1145	GTGACCTGCTGGCCACACCCAGTATACACCTTCGACGATCCAGGCTGTGAACGGCTTACTG	1204
Db	1547	gtagcctatgagcccaacaccccaataacatttgatataccaggcaataatgagtgctta	1606
OY	1205	ACCAAGACCCCTTTGCCCTCACTGTGGCTCTGTGAACATCACACCAACACGACGCTC	1264
Db	1607	gcaagatccctcccccacacgaatgctctgtctcaacaatacacaacaaagctgtccc	1666
OY	1265	CATGCGCAGTTCATCATATCATCAGGTGAGCGGCACCGCTGGACAGCAATTACCGTGTGT	1324
Db	1667	cctccactgtctccataatgacacaggtctcagtcacacatgtagggagatcaactgtcat	1726
OY	1335	GGTCCCAACCGGACACGCCCAATGGCTGATCTGGACTATGAGCTGCAGTACTATGAGA	1384
Db	1727	ggctccagccgagccagcctaataatgatactccgtacataatgataatccgtaactatga	1786
OY	1385	AGGAGCTCAGTGAATACAAAGGCCACAGCCATAAAAGCCCCACCAACACGG-----TCA	1438
Db	1787	aggagcaaaatgaaatcttaactcttcaatgacagagagccagacaaacaaagacatagc	1846
OY	1439	CGGGCTTCAAAGCCGGCCCATATATGTCTTCAGGTGCGGGCAGACACTGTGAGCAGCT	1498
Db	1847	atgggctcagagcccgagatgagtgatgtgtccaggtaaagatctcgaaacgtgtgctgtc	1906
OY	1499	ACGGGCGCTACAGCGGCGCAAGTGTACTTCACAGCATGACAGAGCCGAGTACAGACAA	1558
Db	1907	atggcaagatctcagtgcaagaatgtcgctccagaccttcgaagatgatatcaaatcg	1966
OY	1559	GCATCCAGGAGAAATTTCCCATCATATGGGGCTCGCGGCCGCTGGCGTCTTCCTCA	1618
Db	1967	agctgagagaagaactaacccctgatactcgctggtccctgcaagcgtgggttgatctgtg	2026
OY	1619	TTTGCTGTGTGTTCATCGCCATGCTGTGTAAACAGAGGGGGTTTATAGCGTCTGTACTGG	1678
Db	2027	tgctctcgtgtgcatctcatctgtctctgcagcagaagaagatctaaacaaagagctg	2086
OY	1679	AGTACACGAGACAGCTGCAACACTACACAGTGGCCATTAACCCAGGATGAAGATCT	1738
Db	2087	tgtaacatgataaactctcaagcatatacagacagagccgagctccccagagatgaaatct	2146
OY	1739	ACATCGATCTCTTACTTACCTAGGAGAGCCCCACAGAGCAATGGGGAGTTTGGCAAGGAA	1798
Db	2147	acattgaaccgcttaactatacgaagaccatacgaagcgtgtccggagatgttcgaagaga	2206
OY	1799	TTTGACATCTCTGTGTCAAAATTGAGCAGGTGATCTGGACAGGAGATTGTGGCAGGTCT	1858
Db	2207	ctgaatgtctcttttgtaaaaaatcgaaaggtcatcggagcagggagtlttgagaagagt	2266
OY	1859	GCAATGGCCACCTGAAAGCTCCAGGCAAGAGAGAGATCTTTGTGGCATCAAGAGCTCA	1918
Db	2267	acaagagccgaatctgaagcgtgcagagaagaagatcaatctatgtgcatcaagacccga	2326
OY	1919	AGTGGGCTACACGAGAAACACAGCGCGGAGACTTCTTGAGCAACACTTCATCAGGCGC	1978
Db	2327	aagcttggttactcagagaacacagcgtccggatcttctcgtgcgaagcgtgagatcatagggc	2386
OY	1979	AGTTGACACATCCCAACGTCATCCACCTGGAGGGTGTCTGTGACCAAGACACACTGTGA	2038
Db	2387	agtttgacacatcccaacataatctcgctcagagggtgtgtgtcaacaagagccgactgtca	2446
OY	2039	TGATCATCACGAGATTCATGAGAAATGGCTCCTGTGACATCTTTTCCGGCAAAACATG	2098
Db	2447	tgatcatatcagagatctcagagaatcgtgttgaactcttctccgcgcaaaatgacg	2506

QY	2059	GGCAGTTTCACGATGCATCAGCTGGTGGGACATGCTTGGGGGCAATCGCAGCTGGCATGAAGT	2155
Db	2507	gacagtttcaacggtgacccacgcttgtagggagctgcagagggagcaacgctgcctgagcaagat	2566
QY	2159	ACCTGGCAGACATCAACTATGTTCCACCGTACACCTGGCTGGCCGCAACATCTCTGTCAACA	2218
Db	2567	acctatcttgagatgaaatlaatgtagcaaccggagacctggtctgtaagaaatcttctgtgaaac	2626
QY	2219	GCAACCTGGTCTGCAAGGTGTCCGACTTTTGGCTCTTCAGCGTTTCTAAGAGACATACCT	2276
Db	2627	gcaacctgggtgtgcaaaagtgtctgaccttctgctctctctgcctacacccagagatgaaact	2686
QY	2279	CAGACCCCACTTACACAGCAGTGGCCCTGGGCGGAAAGTTCCCATCCCTGACAGACGCCGG	2338
Db	2687	cagaaaccaacttaacccaagctctctcttgtagggagaaatlaacctgtttagatgtagaacgtccag	2744
QY	2339	AAGCCATCCAGTACCGGAAGTTCACTCGGCCAGTGAATGTGTGGAGCTACGGCATTTGTCA	2398
Db	2747	aagccatctgaccttaacccaagtlttaacgttcaagccagagatcttctgtagcttcaaggatgttca	2806
QY	2399	TGTGGAGAGTCAATTCCTATGAGGGAGCGGGCCCTACAGGGGAGATGACCAACAGAGATGTA	2455
Db	2807	gttggagaaatgaatgtcaatttggtagagagagaccttaacctgagatattgttcaataagaatgttca	2866
QY	2459	TCAATGCCATTGAGCAGAGACTATTCGCTGCGCCACCGCCCATGATGCTGCCAGGCCCTGCG	2515
Db	2867	tcaatgcatctgagcagagactaacacggtgcgcctctctatbtgacctgcagcgttgcctgtgc	2926
QY	2519	ACCAACTCATGCTGAGCTGTGTTGGAGAGAAGAACCGCAACCAACCGGCCCAAGTTCCGCCA	2576
Db	2927	accagcttcaatgctgagactgttctggagaagaatctgaaatbtagccgttccgcttcttgcaagaa	2986
QY	2579	TGTGTCAACACCACTTGAGACAAGATGATCCGCAGTCCCAACAGCCTCAAGAGCATATGGCGCCC	2638
Db	2987	tgcttcaaacaccttggacaagaatgataccggaaacccagctagttcttcaagactgtgtagaacca	3046
QY	2639	TCTCTCTGCGCATCAACCTGCGCTGCTGTGACCGCACAGATCCCGCACTACACCAGCTTTA	2698
Db	3047	tcaacgctgttgccttcccaaacacctgtgttgaacctctatcccaagacttcaacgaccttca	3106
QY	2699	ACACGCTGAGCAGTGTGGAGGCCCATCAAGATGGGGGAGTACAAAGAGAGAGCTTCGCCCA	2758
Db	3107	caacccgtgagatgactggtctaagtgcatacaaatgtgtccagttcaagagaaacagcttccctca	3166
QY	2759	ATGCGCGCTTACACCTCCTTTGACGCTGCTGTCTGAGATGATGATGAGAGACATTTCTCCGGG	2818
Db	3167	cagctgtgttcaactctccctccagcttggttcaaccagatgatacatgaagaccctcttgagaa	3226
QY	2819	TTGGGGTTCATCTTGGCTGGGCCACACGAAAAAATCTCTGAACATATTCAGAGGTGATGCGGG	2876
Db	3227	ttaggggttaacttggcagcgacatacaagaagaatcttcttgacgagcatcacaactcgtatgtagg	3286
QY	2879	CGCAGATGAACAGATTCAGTCTGTGTGGAGGTTTGACA	2915
Db	3287	tccagatgtaaccagctacacgttcgttgaatgtgcattgagaa	3323
RESULT 10			
AA062461			
ID	AA062461 standard; cDNA; 3751 bp.		
XX			
AC	AA062461;		
XX			
DT	09-NOV-1994 (first entry)		
XX			
DE	Human embryonal kinase 2 receptor.		
XX			
KW	Embryonal kinase; HEK; protein tyrosine kinase; PTK; tumour;		
KW	cancer; therapy; amplification; primer; polymerase chain reaction;		
KW	PCR; ss.		
XX			
OS	Homo sapiens.		
XX			

Key	Location/Qualifiers
FT CDS	1..2973
XX	/*tag= a
XX	DE4233782-A.
XX	14-APR-1994.
XX	07-OCT-1992: 92DE-4233782.
XX	07-OCT-1992: 92DE-4233782.
XX	(CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
XX	Holtrich U, Ruebsamen-Walimann H, Strebhardt K;
XX	WPI: 1994-127194/16.
XX	P-PSDB; AAK51899.
XX	Human embryonal kinase 2-receptor protein - useful in tumour
XX	diagnosis and therapy
XX	Claim 4: Page 7-10; 11pp; German.
XX	RNA from human embryonic tissue was isolated. With the use of
XX	primer P6(4) PTK-specific cDNA was synthesised. The cDNA was
XX	amplified using primers P6(4) and N5. A 2097 bp DNA fragment was
XX	obtained. Primers E3, P12 and E6 were then used in the isolation of
XX	the C-terminal of the HEK2 receptor gene.
XX	Sequence 3751 BP; 739 A; 1150 C; 1123 G; 739 T; 0 other;

Query Match 53.5%; Score 1583.4; DB 15; Length 3751;  
 Best Local Similarity 72.6%; Pred. No. 0; Mismatches 766; Indels 33; Gaps 4;  
 Matches 2116; Conservative 0;

10 GCCGTGGAAGAAACGCTAAATGATCCACTACAGCGACTGAGTGGAGTGGTG 69  
 85 ggcgtggaagagagcctctatgacacaaatggttaacatctgagtgctgagcatct 144  
 70 CATCTTCATCAGGTTGGGGAAGAGTGTGCTACGATGAGAAACATGAACAGATCGC 129  
 145 catcttcagatgagtggtggaagagtgagtgctgacgagtgagtgagtgagtgagtg 204  
 130 AGCTACGAGTGTGCAACGCTTGAATGCAAGCAACGAGGAGGAGGAGGAGGAGGAG 189  
 205 acataccaggtgtgtaatgtgagcgagtgcaagcagaacaacatgagtgagtgagtg 264  
 190 ATCCGCGCGCGTGGGCGCCACGATCCAGTGAAGATGAATGATGATGATGATGATG 249  
 265 atctgagcgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 324  
 250 AGCAGATCCCAAGCGTGGCTGCTCTGCAAGAGAGACCTTCAACTTATATATAGAG 309  
 325 aacagatccccaacacaccccgctgctgaagagagacccctcctcctcctcctcag 384  
 310 GGTGATTTGATCGGCGCAACCAAGACCTTCCCACTGATGATGATGATGATGATGATG 369  
 385 ggtgacagagatgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 444  
 370 GTGATATCATTTGACGCGACGAGAGCTTCCAGAGTGGAGCTGGAGCTGGAGCTGATG 429  
 445 gtgagacatctgacacgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 484  
 430 AAAATCAACACGAGTGGGAGCTTCCGACGCTGCTCCGAGCGGCTTCACTGAGCC 489  
 495 --tgtaacaacaggtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 552  
 490 TTCCAGAGTATGAGGCGGAGTGTCCATGAGCGGCTGAGTGTCTTCAACCCAGATGC 549  
 553 ttccagagacaggtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 612

QY 550 CCCCAGATCATCCAAATGGCGCCATCTTCAGGAAACCTGTGCGGGCTGAGAGACA 609  
 613 gcatccacacacgaggtcttcgacatcttcccgagagacctcaactgagtgagggccac 672  
 QY 610 TCGTGTGGCTGCGCGGGGACGTGATGCCAATGCGGAAGAGTGTATACCATC 669  
 673 tctgtgtgcatctgtccctgacatctccttaacgagcggtgagtgagtgagtgagtg 732  
 QY 670 AAGCTCTACTGTAAAGGAGGAGGAGTGGCTGTGCGGCTGAGGAGGAGGAGGAGGAG 729  
 733 aagctctactgtcaacgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 792  
 QY 730 GCAAGCTTCGAGGCGTGTGGAATGGCAGCGCTGCGGAGTGTTCATGAGACTTC 789  
 793 accgagcatgagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 852  
 QY 790 AAGGCCACACAGG3GATGAGGCTGTGACCATGTGCTTCAACAGCGGAGCAGCTCT 849  
 853 aagcgagagcagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 912  
 QY 850 GAAGGGGCGACCAATGTGTGCTGCGGAGTGTGCTGAGAGAGAGAGAGAGAGAGAG 909  
 913 ctagcgccagcatctgacatctgacatctcaataacttcaactgagtgagtgagtgag 972  
 QY 910 GACATGCGCTGTGACAAACCATCCCTCGCGCCCGAGGCTGTGATTCAGTGTCAATGAG 969  
 973 gaaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1032  
 QY 970 AACTCCCTCATGCT3GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1029  
 1033 acctcaactgtactctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1092  
 QY 1030 TACAACTCATGCT3AAGAGCTGTGAGGCTGGGCGGGG-----TGCGCTACCGGCTG 1083  
 1093 tacaatgtactctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1152  
 QY 1084 GGGGACATGTATACAT3AAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1143  
 1153 gatgacagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1212  
 QY 1144 AGTGACCTGTGGCGCCACACCCAGTACCTTGGAGATCCAGGCTGTGAACGGCGTTACT 1203  
 1213 agcatctgtgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1272  
 QY 1204 GACCAAGCGGCTT3TCCGCTTCAGTGTGAGTGAATCAACCAACCAACCAACCAAC 1263  
 1273 ggcagagagcctctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1332  
 QY 1264 CCATCGGAGCTGT3ATCATGATCATGAGTGAGCGGACCGTGGAGACATATACCTGTG 1323  
 1333 cgtctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1392  
 QY 1324 TGTGTCAGCGGAG3CAGGCCAATGGCGTGTATCTGTGACTATGAGTGTGAGTGTGAG 1383  
 1393 tgggacaccccaagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1452  
 QY 1384 AAGGAGCTCATGAT3ATCAACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1443  
 1453 aagagagagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1512  
 QY 1444 CTCAAAGCGGCGC3ATCATGTCTTCAGAGTGGGAGCAGCAGTGTGAGGCTACAGGG 1503  
 1513 ctccgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1572  
 QY 1504 CGCTACAGCGGAG3ATGATCTTCAGAGCAGCAGTATACAGAGCCAGTATACAGAGCA 1561  
 1573 cagtgagagcgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1632  
 QY 1562 -TCCAGAGAGAGT3CCACATCATGAGGCTGTGCGGCTGAGGCTGTGCTCATAT 1620  
 1633 ctccagagagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1692  
 QY 1621 GCTGTGTTGTCTAT3CCATGCTGTGTATACAGAGCGGGGCTTGAAGCGTGTGACTGAG 1680

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Db 1693 gctgtcgtgtgtatcgtatcgtatcgtctcgtcctcgaagcagcgacagcgctcgtatcgtgag 1752
Oy 1681 TACAGGAGACAGCTGCACACTACACAGATGAGCAGATTAACCCAGGATGAAGATCTAC 1740
Db 1753 tacacggagaagctgcagagct-----acatgctccctcggaatgaaagttatc 1800
Oy 1741 ATCGATCCCTTTACCTACAGAGACCCCAACGAGCAGTGCAGGAGCTTTGCCAAGAAATT 1800
Db 1801 attgacccctttacctaaggaacccctaaatgagctgtcgtgaggtcttgccaagaagatc 1860
Oy 1801 GACATCTCCTGTGTAAATTGAGCAGGATGATCGAGAGGAGGAGCTTTGGCAGAGCTGAC 1860
Db 1861 gacggtctcgtgtcgaagaatcgaagaggtgcagagagctcggagaaatctcggagaaagctg 1920
Oy 1861 AGTGCCACCTTGAGCTGCCAGCAGAGAGAGATCTTTGTGGCCATCAGACGCTCAAG 1920
Db 1921 cgttgctcgaactgaacagacgtcgtccgagaggtgtcttggtgccaatgaagcgtcgtgag 1980
Oy 1921 TCGGGCTACAGCAGACAGCAGCGCGGAGCTTCTGAGCAGGAAGCTCCATCATGGGCCAG 1980
Db 1981 gctggctacacgaagagcgagcggtggtcctcctaagcgaggtccatcatalggtcag 2040
Oy 1981 TTGCAACATCCCAACGATCATCCATCAGGAGGAGGTGTGTGAGCAAGACACATCTGTATG 2040
Db 2041 ttgtgtaccccaataataataatcgcgtcgtcgtgaggtgtgtgtcacaagaatcgcgcagatc 2100
Oy 2041 ATCATCACCGAGTTTCATGAGAGATGCTCCCTGAGCTCTTTCTCGGCAAAACGATGGG 2100
Db 2101 atccctacgtgtcgtatgaaacgtcgcgcgtcgtcctcctcgtcgtcgtcgtcgtcgtcgt 2160
Oy 2101 CAGTTCACAGCATCATCCAGCTGTGGGAGTGTCTCGGGGAGTATCGAGCTGAGTGAAGTAC 2160
Db 2161 cagttcacggtcacaacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2220
Oy 2161 CTGGCAGACATGAATATGTTTACCGGTGAGCTGTGGCTGCGCCAGACATCTCTGTCAAGAGC 2220
Db 2221 ctgttcgagagtaagtaataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2280
Oy 2221 AACCTGGCTCTCAAGGTGTGAGCTTTGGGCTCTTCACGCTTTTCTAGAGAGACATACCTCA 2280
Db 2281 aacctgtgtcgaagctcgaagctcgtcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 2340
Oy 2281 GACCCACCTTACACAGAGCTGTGGGAGGAGTTCCTCCATCCCTGTGACAGCCCGGAA 2340
Db 2341 gattctacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 2400
Oy 2341 GCCATCCAGTACCGAAGTTCACCTCGGCTGAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2400
Db 2401 gcatagacctatcgaaagttcaacttcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2460
Oy 2401 TGGGAGGTGATGTCTTATGGGAGCGGCGCTTATGAGCATGACCAACAGATGTATC 2460
Db 2461 tgggaggttcatagagctatgagagcgacccctacgtgagcatgagcaacacagatgcatc 2520
Oy 2461 AATGCACTTGAGCAGGAGTATCGGCTGTGCACCGCCCATGAGCTCCCGAGCGCCCTGCAC 2520
Db 2521 aatgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2580
Oy 2521 CMACTCATGTGAGTGTGTGAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2580
Db 2581 cagctcatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2640
Oy 2581 GTCAACAGCTAGACAGATGATCCGAATCCCAACAGCTCAAAAGCCTGAGCGCCCTC 2640
Db 2641 gtcaataccctgtgacaagctcatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 2700
Oy 2641 TCCCTGTGAGCAGCAGCGCGCTGTGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2700
Db 2701 cagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2760
Oy 2701 ACGGTGACGAGTGTGTGAGGCGCATCAAGATGGGAGTGAACAAGAGAGCTTCCGAAT 2760

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Db 2761 acagttgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2820
Oy 2761 GCCGCTTACCTCTCTTGTGAGTGTGTGTGAGATGATGAGAGGAGATCTCTCCGGTT 2820
Db 2821 gctgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2880
Oy 2821 GGGGTCACTTTGCTGTGCGCACAGAAAAATCTGAACTATTCAGTATTCAGTATTCAGTATTCAG 2880
Db 2881 ggggtcacccctgtgcgcgcacacagagaagatcctcgtgagcagatccagagatcgtcgtgt 2940
Oy 2881 CAGATGAACCAAGATTTCATCTGTGTGAGGTTGACA 2915
Db 2941 cagatgaaccagagcgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2975

RESULT 11
AAQ90656
ID AAQ90656 standard; cDNA: 3546 BP.
AC AAQ90656;
AC AAQ90656;
DT 11-NOV-1995 (first entry)
XX
DE Eph-related PTK Cdk10 cDNA.
XX
KW Cdk10; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
KW prognosis; ss.
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT CDS 2..2923
FT /*tag= a
PN W09515375-A.
PD 08-JUN-1995.
PE 07-SEP-1994; 94WO-US10140.
PF 03-DEC-1993; 93US-0162809.
PR (JOL-) LA JOLLA CANCER RES FOUND.
PA
XX Pasquale EB, Sajjad1 FG;
XX
XX WPI: 1995-215256/28.
XX P-PSDB: AAR75708.
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
PS
XX
XX Claim 2; Page 63-67; 129pp; English.
XX
CC Novel Eph-related PTK cDNA clone Cdk10 (given in AAQ90656) and a
CC variant clone, Cdk10+ (AAQ90658), whose product contains a 15-amino
CC acid insertion in the juxtamembrane domain, were isolated from a
CC chick embryo library in lambda gtl1. Cdk10 and Cdk10+ may
CC originate from the same gene by alternative splicing. Cdk10
CC expression was prominent in the kidney, and to a lesser extent in
CC the lung.
XX
XX
XX Sequence 3546 BP; 742 A; 1100 C; 1031 G; 673 T; 0 other;

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Query Match 53.4%; Score 1581.6; DB 16; Length 3546;  
Best Local Similarity 73.1%; Pred. No. 0;  
Matches 2114; Conservative 0; Mismatches 734; Indels 42; Gaps 5;

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Oy 43 GCACAGTGTGAGTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 102
Db 59 gtgacctgtgagctgtgcatgagacacacacacacacacacacacacacacacacacacacacac 118

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Db 2255 ttccggctctcccgcttcttttgaggatgatccagccgaccccaactacaccagctccctg 2314  
 QY 2305 GCGGGAAGTTCCCATCCGCTGACAGACCCCGGAGGCATCATGATCCGGAAGTTGACC 2364  
 Db 2315 ggaaggcaagatcccatcagtgagcagctctctgagccatccgctacccaatactacg 2374  
 QY 2365 TCGCGAGATGATGTGAGTACGAGCATTTGTCACTGTGGAGGTGATGCTTATGAGGAG 2424  
 Db 2375 tcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2434  
 QY 2425 GCGCCCTACTGGAGATGACCAACAGGATGATCAATGATGATGATGATGATGATGATGAT 2484  
 Db 2435 cgacctactcggacatctccacacagatgtagtcaacgcggtgagcagagatccagc 2494  
 QY 2485 CTGCGACCGCCCATGAGTATGCGCCGACGCGCTGACCACTCATGATGATGATGATGATGAT 2544  
 Db 2495 ctgcacaccccccagactcgcacacagcagcagcagcagcagcagcagcagcagcagcag 2554  
 QY 2545 AAGGACCGCAACACCGCCCAAGTGTGCGCAATTTGTCAACAGCGTACAGCAAGATGATG 2604  
 Db 2555 cgggacccgcaacccctgcgcccagatctgcacagatctgcacacagcagcagcagcagc 2614  
 QY 2605 CGCAATCCCAACAGCTCTCAAGCCATGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2664  
 Db 2615 cgcacatctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2674  
 QY 2665 CTGACCGCAGATGCCCGCTACACAGCTTACACAGCTGACAGTGTGAGAGGCC 2724  
 Db 2675 ctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2734  
 QY 2725 ATCAAGATGGGAGATGACAGAGAGCTTCCGCAATGCCGCTTCACTCTCTCTCTCTCTCT 2784  
 Db 2735 atcaaatctggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2794  
 QY 2785 GTGCTCAGATGATGATGAGGAGCATTTCCCGGTTGGGTTGCTTGTGCTGCTGCTGCTGCT 2844  
 Db 2795 gtgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2854  
 QY 2845 AAAAAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2904  
 Db 2855 aagaagatctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2914  
 QY 2905 GAGGTTTGAC 2914  
 Db 2915 caggtctgac 2924  
 RESULT 12  
 AA090658  
 ID AA090658 standard; cDNA; 3591 BP.  
 AC AA090658;  
 XX  
 DT 11-NOV-1995 (first entry)  
 DE Eph-related PTK Cdk10+ cDNA.  
 KW Cdk10+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
 KW prognosis; ss.  
 OS Gallus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 2..2968  
 FT /tag- a  
 XX MO9515375-A.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 07-SEP-1994; 94MO-US10140.  
 XX  
 PR 03-DEC-1993; 93US-0162809.

XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Pasquale EB, Sajjad RG;  
 XX  
 DR MPI: 1995-215256/28.  
 DR P-PSDB: MAR75710.  
 XX  
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 XX cancer.  
 PS  
 PS Claim 2; Page 78-82; 129pp; English.  
 CC  
 CC Novel Eph-related PTK cDNA clone Cdk10 (given in AA090656) and a  
 CC variant clone, Cdk10+ (AA090658), whose product contains a 15-amino  
 CC acid insertion in the juxtamembrane domain, were isolated from a  
 CC chick embryo library in lambda g11. Cdk10 and Cdk10+ may  
 CC originate from the same gene by alternative splicing. Cdk10  
 CC expression was prominent in the kidney, and to a lesser extent in  
 CC the lung.

Sequence 3591 BP: 753 A; 1112 C; 1042 G; 684 T; 0 other;

Query Match 52.1%; Score 1543.4; DB 16; Length 3591;  
 Best Local Similarity 72.3%; Pred. No. 0;  
 Matches 2114; Conservative 0; Mismatches 746; Indels 63; Gaps 6;

QY 43 GCGACTGCTGCTGGCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 102  
 Db 59 gtgaccccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 118  
 QY 103 TACGATGAGAAATGAAACAGATCCGACGATACGATGATGATGATGATGATGATGATGATGAT 162  
 Db 119 taagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 178  
 QY 163 CAGAACACTGCTGATGAGAACAAATTTATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 222  
 Db 179 cagaacacactgctcgcacacagctcattcagcagcagcagcagcagcagcagcagcagcag 238  
 QY 223 GAGATGAGTTTTCGGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282  
 Db 239 gagctgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 298  
 QY 283 GAGACCTTCAACCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342  
 Db 299 gagacctcaacctctctcattatgagcagcagcagcagcagcagcagcagcagcagcagc 358  
 QY 343 AACTGATGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402  
 Db 359 tcttgatgagagacccctataccaagtgagatacaattgctcagcagcagcagcagcagc 418  
 QY 403 CAGGTGACCTGGTGGCGCGCTCATGAAATCAACACCGAGTGGAGCTTGGACT 462  
 Db 419 aaactgagagctccgcg-----tggaacacacagcagcagcagcagcagcagcagcagc 466  
 QY 463 GTGTCCCGACGCGCTTACCTGCTTCCAGAGCTATGCGCGCTGATGATGATGATGATGATGAT 522  
 Db 467 ctctccaagaatgcttctatctgcttccagagcccggtggtcagcagcagcagcagcagc 526  
 QY 523 GCGTGGGATGCTTATACCGCAAGTGGCGCGCTCATGCAAGTGGCGCGCTTGGACT 582  
 Db 527 tcgctcgggcttctcacaagaatgctcacaacacacacacacacacacacacacacacacac 586  
 QY 583 GAAACCTGTGCGGCGCTGAGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642  
 Db 587 gagaacctcaacggggcctgagccacgctcgtgctcagcagcagcagcagcagcagcagcag 646  
 QY 643 AATGGGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 702  
 Db 647 aacgcagtgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 706  
 QY 703 GTGCCATCGGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 762



Db	707	gtgcctcttggagagcgtgcacgctgtgcctcgggtatcagagccagccatgtagaggtatcccaag	766
Qy	763	TGCGAGGTTTTCATGTCAGTCTTTCAAGGCCAACCCAGGGATGAGCCTGTATCCAC	822
Db	767	tgccaagatcgtcgccggggagcttcaaatccaagcaggcgagggccctctccccc	826
Qy	823	TGTCCCATCAACAGCCCGGACCACTTCTTGAAAGGGGCCCAACAACTTGTCTCCGCAATGGC	882
Db	827	tgccttcccaacaacgcagccacacacgcgggggagcagcagctctcatatgttcgaagcgc	886
Qy	883	TACTACAGAGCAGACTGTGACCCCTTGACATGTGCCCTGACACAACTATCCCTCCGCGCC	942
Db	887	tctctcagagcagatcggaaccccgacagcgcctgcacagctgtgcctcgaagcccca	946
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Db	1667	tgtctcagaagaaaggatgtgttaactgatacaactctctctgtctctcttggcgaaagcag	1726
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RESULT 14			
ID	AAQ90982	standard; cDNA to mRNA; 4027 BP.	
XX	AAQ90982;		
AC	24-NOV-1995	(first entry)	
DT	Protein p140 cDNA from rat skeletal muscle myoblast cell line L6.		
DE	Protein p140; insulin; tyrosine phosphorylation; ss.		
XX	Rattus rattus.		
KW			
XX			
OS			
XX	Key	Location/Qualifiers	
FT	CDS	262..3243	
FT		/*tag- a	
XX	EP659883-A.		
XX	28-JUN-1995.		
PD	24-NOV-1994;	94EP-0118524.	
XX	24-NOV-1993;	93JP-0315806.	
XX	(ONOI ) ONO PHARM CO LTD.		
XX	Kitagawa K, Ohno H, Tajima H;		
XX	WPT; 1995-226291/30.		
DR	P-PSDB; AAR75844.		
XX	Isolated protein p140 polypeptide - and treatment of diabetes based		
PT	on tyrosine phosphorylation of protein p140.		
XX	Example; Page 28-33; 42pp; English.		
PS			
XX			





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Wed Jul 11 10:25:37 2001

us-09-378-759-10.rng

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[illegible]

Search completed: July 10, 2001, 18:40:55  
Job time: 6512 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 10, 2001, 16:06:53 ; Search time 86.52 Seconds  
(without alignments)  
6342.362 Million cell updates/sec

Title: US-09-378-759-10

Perfect score: 2962 1 CTGCTCGCCCGCGTGAGAGA.....CCAGCCCGCCCTCTCTGC 2962

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Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Issued\_Patents\_NA.\*  
2: /cgn2\_6/ptodata/2/1na/5A.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/1na/5B.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/1na/6A.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/1na/6B.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/1na/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2962	100.0	2962	2	US-08-449-645A-10
2	2962	100.0	2962	2	US-08-702-367A-10
3	2962	100.0	2962	5	PCT-US95-04681-10
4	2498	84.3	3105	4	US-08-542-635-1
5	2185.6	73.8	4049	1	US-08-162-809-17
6	2127.6	71.8	4097	1	US-08-162-809-11
7	1581.6	53.4	3546	1	US-08-162-809-9
8	1543.4	52.1	3591	1	US-08-162-809-13
9	1526.4	51.5	4027	1	US-08-348-143-3
10	1526.4	51.5	4027	1	US-08-348-143-4
11	1526.4	51.5	4027	1	US-08-571-785-3
12	1526.4	51.5	4027	1	US-08-571-785-4
13	1520.8	51.3	2982	1	US-08-348-143-2
14	1520.8	51.3	2982	1	US-08-571-785-2
15	1459.6	49.6	3133	1	US-08-162-809-1
16	1196.8	40.4	3776	1	US-08-436-004-5
17	1075	36.3	3969	1	US-08-222-616-23
18	1075	36.3	3969	1	US-08-222-616-23
19	1075	36.3	3969	1	US-08-436-004-5
20	1075	36.3	3969	5	PCT-US95-04228-23
21	1075	36.3	3969	5	PCT-US95-08812-5
22	1037.2	35.0	3116	2	US-08-449-645A-14
23	1037.2	35.0	3116	2	US-08-702-367A-14
24	1035.6	35.0	3116	5	PCT-US95-04681-14
25	1035.6	35.0	3348	5	US-08-222-616-34
26	1035.6	35.0	3348	5	PCT-US95-04228-34
27	992.8	33.5	3254	1	US-08-162-809-15

28	956.8	32.3	3162	2	US-08-449-645A-12	Sequence 12, Appl
29	956.8	32.3	3162	2	US-08-702-367A-12	Sequence 12, Appl
30	956.8	32.3	3162	5	PCT-US95-04681-12	Sequence 12, Appl
31	949.4	32.1	2820	1	US-08-162-809-5	Sequence 5, Appl1
32	943.8	31.9	4304	5	PCT-US96-00419-1	Sequence 1, Appl1
33	909.6	30.7	3132	1	US-08-167-919A-9	Sequence 9, Appl1
34	909.6	30.7	3132	3	US-08-715-106-9	Sequence 9, Appl1
35	907	30.6	4529	2	US-08-449-645A-16	Sequence 16, Appl
36	907	30.6	4529	2	US-08-702-367A-16	Sequence 16, Appl
37	907	30.6	4529	5	PCT-US95-04681-16	Sequence 16, Appl
38	869	29.3	3906	2	US-08-469-537A-102	Sequence 102, App
39	697.2	23.5	3592	2	US-08-162-809-3	Sequence 3, Appl1
40	661.2	22.3	3059	1	US-08-162-809-21	Sequence 21, Appl
41	629.6	21.3	3056	1	US-08-162-809-19	Sequence 19, Appl
42	605.2	20.4	3125	1	US-08-442-248-1	Sequence 1, Appl1
43	572.8	19.3	4165	1	US-08-440-815-1	Sequence 1, Appl1
44	572.8	19.3	4165	1	US-08-440-815-1	Sequence 1, Appl1
45	564	19.0	4322	1	US-08-673-789-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-449-645A-10  
; Sequence 10, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RMW  
; STREET: 1840 DeWittland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,645A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2962 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2913  
; US-08-449-645A-10

Query Match 100.0% Score 2962; DB 2; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TGGATGTCATCTCCATCAGGCTGAGAGAGGTGAGTGGCTACGATGAGAACATGAAAC 120

|||||  
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Db 2701 ACGGTGACAGATGGCTGGAGGCGCATCAAGATGGGCGAGTCAAGAGAGATGTCCCAAT 2760  
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Db 2761 GCCGCTTACCTCTTGTGACGTCTGTCTCAGATGATGAGAGACATTCCTCGGGTT 2820  
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RESULT 2  
US-08-702-367A-10  
; Sequence 10, Application US/08702367A  
; Patent No. 5981246  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine  
; ;  
; TITLE OF INVENTION: Kinases  
; ;  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702.367A

;; FILING DATE: 435  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winters, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-287  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 2962 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..2913  
;; US-08-702-367A-10  
  
Query Match 100.0%; Score 2962; DB 2; Length 2962;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 CTGCTCGCGCGGTGAGAAACGCTTAATGACTCCACTACAGCAGTGTGAGCTGGGC 60  
Qy 61 TGGATGTCATCTCTCATCAGGTGGGAGAGTGAAGTGTGATGAGAACATGAAAC 120  
Db 61 TGGATGTCATCTCTCATCAGGTGGGAGAGTGAAGTGTGATGAGAACATGAAAC 120  
Qy 121 ACGATCCGACGTACCAGTGTGCAACGTGTGAGTCAAGCCAAACACCTGGCTAGG 180  
Db 121 ACGATCCGACGTACCAGTGTGCAACGTGTGAGTCAAGCCAAACACCTGGCTAGG 180  
Qy 181 ACCAAGTTATCCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGAATTTGCGTG 240  
Db 181 ACCAAGTTATCCGCGCGGTGGGCGCCACCGCATCCAGTGGAGATGAATTTGCGTG 240  
Qy 241 CGTGAATCAGCAGATCCCGAGCTGCTGCTCTGCAAGAGACCTTCAACCTTAT 300  
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Qy 361 TGGGTGAAGGTGATACCATTTGACGCCAGCAGAGACCTTCCAGGTGAGCTGGTGC 420  
Db 361 TGGGTGAAGGTGATACCATTTGACGCCAGCAGAGACCTTCCAGGTGAGCTGGTGC 420  
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Qy 601 GAGACACATCGCTGTGCTGCTCCGCGGACAGCTGATGCGCAATGCGGAAGGTGAT 660  
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Qy 661 GTACCATCAAGCTTACTGTAAAGGAGAGGAGAGTGTGCTGCGGAGCTGCTG 720  
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QY	781	GGGACTTTCAGAGCCAAACCAAGGGGATGAGCGCTGTACCCACTGTCCTCATCAACAGCCGG	840
Db	781	GGGACTTTCAGAGGGCAACCAAGGGGATGAGCGCTGTACCCACTGTCCTCATCAACAGCCGG	840
QY	841	ACCACTTGTGAAGGGGCGACCAACTGTGTGTGGCGGAATGGCTACTACAGACACCGTG	900
Db	841	ACCACTTGTGAAGGGGCGCACCAACTGTGTGTGGCGGAATGGCTACTACAGACACCGTG	900
QY	901	GACCCCTGGACATGACCTTGACAAACCATCCCTCGCGGCCCCAGGCTGTGATTTCCAGT	960
Db	901	GACCCCTGGACATGACCTTGACAAACCATCCCTCGCGGCCCCAGGCTGTGATTTCCAGT	960
QY	961	GTCAATGAGACTCCCTCCTATGTCTGGATGGAGACCCCTCCCGGACCTCCGGAGCCGAGAG	1020
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QY	1021	GACCTGCTCAACAATCATCTGCAAGAGCTGTGGCTCGGGGCGGGGTGCTGTGACCCGC	1080
Db	1021	GACCTGCTCAACAATCATCTGCAAGAGCTGTGGCTCGGGGCGGGGTGCTGTGACCCGC	1080
QY	1081	TGGCGGGACATGTACAGTACGACACCAAGCCGCACTAGGCTGTACCGAGCCACGCAATTAC	1140
Db	1081	TGGCGGGACATGTACAGTACGACACCAAGCCGCACTAGGCTGTACCGAGCCACGCAATTAC	1140
QY	1141	ATCAGTGCACCTGTGAGCCCAACACCAAGTACACCTTGAGATGCAGGCTGTGAACGCGCTT	1200
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QY	1201	ACTGACCAAGAGCCCTTCTGCGCTCAGTTCCGCTGTGTGAATCATCAACCAACGAGCA	1260
Db	1201	ACTGACCAAGAGCCCTTCTGCGCTCAGTTCCGCTGTGTGAATCATCAACCAACGAGCA	1260
QY	1261	GCTCATGCGGAGTGTCCATCATGATCATCAGGTGAGCGGACCGTGGAGCATTAACCGTG	1320
Db	1261	GCTCATGCGGAGTGTCCATCATGATCATCAGGTGAGCGGACCGTGGAGCATTAACCGTG	1320
QY	1321	TCGTGTGCCAGCCGGACCAAGCCCAATGGCGTGATCCTGAGATGAGCTGCACTACTAT	1380
Db	1321	TCGTGTGCCAGCCGGACCAAGCCCAATGGCGTGATCCTGAGATGAGCTGCACTACTAT	1380
QY	1381	GAGAAAGAGCTCAATGTAGTACAAAGCCCAACGCCATATAAAAGCCCAACCAACGSTCACG	1440
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QY	1441	GGCCTCAAAAGCCGGCGCATCTATGTCTTCGAGTGCAGGACGACACTGTGGACAGCTAC	1500
Db	1441	GGCCTCAAAAGCCGGCGCATCTATGTCTTCGAGTGCAGGACGACACTGTGGACAGCTAC	1500
QY	1501	GGGCGCTACAGCGGCAAGATGTACTTCCAGACCATACGAAGACCGATACAGCAAGC	1560
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QY	1561	ATTCAGAGGAAGTGGCCACTCATCATCGGCTCTCGGCCGGCGGCGTGGTCTCTCTCATTT	1620
Db	1561	ATTCAGAGGAAGTGGCCACTCATCATCGGCTCTCGGCCGGCGGCGTGGTCTCTCTCATTT	1620
QY	1621	GCTGTGGTGTCAATCGGCATCGTGTGTAAACAGACGGGGGTTTGAACGTCGTACTCGAG	1680
Db	1621	GCTGTGGTGTCAATCGGCATCGTGTGTAAACAGACGGGGGTTTGAACGTCGTACTCGAG	1680
QY	1681	TACACGGACAAAGCTGCACAACTACACCAAGTGGCCACATTAACCCAGGCAATGAAGTCTAC	1740
Db	1681	TACACGGACAAAGCTGCACAACTACACCAAGTGGCCACATTAACCCAGGCAATGAAGTCTAC	1740
QY	1741	ATCAGTCCTTTCACATCTACGAGGAGCCCAACGAGAGCAAGTGCAGGGAATTTGCCAAGAAAT	1800
Db	1741	ATCAGTCCTTTCACATCTACGAGGAGCCCAACGAGAGCAAGTGCAGGGAATTTGCCAAGAAAT	1800
QY	1801	GACATCTCTCTGTGTCAAAATTGACAGAGTGTATGGACAGGGGAGATTGGCGAGCTGCG	1860
Db	1801	GACATCTCTCTGTGTCAAAATTGACAGAGTGTATGGACAGGGGAGATTGGCGAGCTGCG	1860

QY	1861	AGTGGCCACCTGGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCATCAAGACGTCTAAG	1920
Db	1861	AATTGGCCACCTGAAGCTGCCAGGCAAGAGAGATCTTTGTGGCATCAAGACGTCTAAG	1920
QY	1921	TGGGGCTACAGGGAGGAAGCAGCGCGGGAGATTCTCTAGGGAAGCCTCCATCATGGGCGAG	1980
Db	1921	TGGGGCTACAGGGAGGAAGCAGCGCGGGAGATTCTCTAGGGAAGCCTCCATCATGGGCGAG	1980
QY	1981	TTTGCACATCCCAACGTCATCCACCTTGAGGGGTGTCTGACCAAGACACACACTGTGTATG	2040
Db	1981	TTTGCACATCCCAACGTCATCCACCTTGAGGGGTGTCTGACCAAGACACACACTGTGTATG	2040
QY	2041	ATCATCACCCGAGTTCTATGAGAGATGGCTCCCTGGAATCTTTCTCCGGCAAAAGATATGG	2100
Db	2041	ATCATCACCCGAGTTCTATGAGAGATGGCTCCCTGGAATCTTTCTCCGGCAAAAGATATGG	2100
QY	2101	CAGTTCAACAGTCATCCAGCTGGTGGGAGTCTTTCCGGGGATGAGCAGCTGGCATGAATGAC	2160
Db	2101	CAGTTCAACAGTCATCCAGCTGGTGGGAGTCTTTCCGGGGATGAGCAGCTGGCATGAATGAC	2160
QY	2161	CTGGCAGACATGAACATATGTTTCAACCGGTGACCTGGCTGGCCCGCAACATCCTGTCTAACAGC	2220
Db	2161	CTGGCAGACATGAACATATGTTTCAACCGGTGACCGTGGCTGGCCCGCAACATCCTGTCTAACAGC	2220
QY	2221	AACTGCTGCTCAAGAGTGTGTGGACTTTGGGCTCTACGCTTTCTATGAGAGAGATATCTCA	2280
Db	2221	AACTGCTGCTCAAGAGTGTGTGGACTTTGGGCTCTACGCTTTCTATGAGAGAGATATCTCA	2280
QY	2281	GACCCCACTTACACACTGTGGCCGTGGGGGGGAAATGCCCATCGGTGGACAGCCCGGAA	2340
Db	2281	GACCCCACTTACACACTGTGGCCGTGGGGGGGAAATGCCCATCGGTGGACAGCCCGGAA	2340
QY	2341	GCCATCCAGTACCCGAGATTACCTCGTGGCCAGTGAATGTTGGAGCTACGGCATTTGTATG	2400
Db	2341	GCCATCCAGTACCCGAGATTACCTCGTGGCCAGTGAATGTTGGAGCTACGGCATTTGTATG	2400
QY	2401	TGGGAGGTGATGTCTATGGGGAGACGGCCCTACTGGGACATGACCACACAGATGTATAC	2460
Db	2401	TGGGAGGTGATGTCTATGGGGAGACGGCCCTACTGGGACATGACCACACAGATGTATAC	2460
QY	2461	AATGCGCATTAGGCAAGACATATGGGCGTGGCCACCGCCCATATGAACTGGCCGAGGCCCTGCAC	2520
Db	2461	AATGCGCATTAGGCAAGACATATGGGCGTGGCCACCGCCCATATGAACTGGCCGAGGCCCTGCAC	2520
QY	2521	CAACTCATGCTGGAATCTTGTGGCAAGAGACCGCAACACACCGGCCCAATTTGGCCCAATT	2580
Db	2521	CAACTCATGCTGGAATCTTGTGGCAAGAGACCGCAACACACCGGCCCAATTTGGCCCAATT	2580
QY	2581	GTCAACAACGCTAGAATAGATATCCGCAATCCCAACAGCCTCAAGAGCCATGGGCCCTCTC	2640
Db	2581	GTCAACAACGCTAGAATAGATATCCGCAATCCCAACAGCCTCAAGAGCCATGGGCCCTCTC	2640
QY	2641	TCTCTGTGGCATCAATCTGCGCGTGTCTGAGACCGCAGAGATCCCGACTACACAGCTTTAAC	2700
Db	2641	TCTCTGTGGCATCAATCTGCGCGTGTCTGAGACCGCAGAGATCCCGACTACACAGCTTTAAC	2700
QY	2701	ACGGGAGCGAGTGTGCTGGAGGCGCATCAAGATGGGGGAGTCAAGAGAGTTCGGCAAT	2760
Db	2701	ACGGGAGCGAGTGTGCTGGAGGCGCATCAAGATGGGGGAGTCAAGAGAGTTCGGCAAT	2760
QY	2761	GCGGCGCTTCACTCTCTTTGACGTCGTGTCTCAGATGATGATGAGAGACATTTCTCGGGTT	2820
Db	2761	GCGGCGCTTCACTCTCTCTTTGACGTCGTGTCTCAGATGATGATGAGAGACATTTCTCGGGTT	2820
QY	2821	GGGGTCACTTTGGCTGGCCACCGAAGAAAAAATCTCGAACAGATATCAAGTGTATCGGGCG	2880
Db	2821	GGGGTCACTTTGGCTGGCCACCGAAGAAAAAATCTCGAACAGATATCAAGTGTATCGGGCG	2880
QY	2881	CAGATGAACAGAGATTCAGTGTGGGAGGTTTACATTCACCTGCCTGGGGCTCACTTTTC	2940
Db	2881	CAGATGAACAGAGATTCAGTGTGGGAGGTTTACATTCACCTGCCTGGGGCTCACTTTTC	2940
QY	2941	CTTCCAAAGCCCGCCCTCTGCG	2962

Db 2941 CTCACAGCCCCCGCCCTCTGC 2962

## RESULT 3

PCT-US95-04681-10

Sequence 10, Application PC/TUS9504681

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04681

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2962 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2913

PCT-US95-04681-10

Query Match 100.0%; Score 2962; DB 5; Length 2962;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCCGCCCGCCGGAAGAAAGCCTAATGACATCCACTACAGGACTGCTGAGCTGGC 60  
Db 1 CTCCTCCGCCCGCCGGAAGAAAGCCTAATGACATCCACTACAGGACTGCTGAGCTGGC 60  
QY 61 TGGATGATGATCTCTCATCAGAGGTGGGAAGAGGTGAGTGCATGAGTAATCATGAAAC 120  
Db 61 TGGATGATGATCTCTCATCAGAGGTGGGAAGAGGTGAGTGCATGAGTAATCATGAAAC 120  
QY 121 ACATATCCGACGATACAGAGGTGTCACAGTGTGATGATCAAGCCAGAACTGGCTACGG 180  
Db 121 ACATATCCGACGATACAGAGGTGTCACAGTGTGATGATCAAGCCAGAACTGGCTACGG 180  
QY 181 ACCAAGTTATCCGGGCGCGTGGGGCCACCGCATCCAGCTGGAGATGAAGTTTTCGGTG 240  
Db 181 ACCAAGTTATCCGGGCGCGTGGGGCCACCGCATCCAGCTGGAGATGAAGTTTTCGGTG 240  
QY 241 CGTGACTGACAGCATCCCGAGCGTCTGGCTCTGCAAGAGAGACTTCAACCTCTAT 300  
Db 241 CGTGACTGACAGCATCCCGAGCGTCTGGCTCTGCAAGAGAGACTTCAACCTCTAT 300  
QY 301 TACTATGAGGCTGACTTTGACTGGGCGACCAAGACTTCCCAACTGATGAGAAATCCA 360  
Db 301 TACTATGAGGCTGACTTTGACTGGGCGACCAAGACTTCCCAACTGATGAGAAATCCA 360  
QY 361 TGGGTGAAGGTGATACCATTTGACAGCGAGAGAGCTTCTCCAGGTGAGACTGGTGGC 420

Db 361 TGGGTGAAGGTGATACCATTTGACAGCGAGAGCTTCTCCAGGTGAGACTGGTGGC 420  
QY 421 CGGCTCATGAAATCAACACAGGAGTGGAGCTTGGACCTGATGCCGAGCGGCTTC 480  
Db 421 CGGCTCATGAAATCAACACAGGAGTGGAGCTTGGACCTGATGCCGAGCGGCTTC 480  
QY 481 TACCTGGCTTCCAGGACTATAGGCGGTGATGCTCCATCGCGGTGCTTCTAC 540  
Db 481 TACCTGGCTTCCAGGACTATAGGCGGTGATGCTCCATCGCGGTGCTTCTAC 540  
QY 541 CGCAAGTCCCGCCGATCATTCAGAAATGGCGCCATCTTCCAGGAACCTCTCGGGGCT 600  
Db 541 CGCAAGTCCCGCCGATCATTCAGAAATGGCGCCATCTTCCAGGAACCTCTCGGGGCT 600  
QY 601 GAGACACATCGCTGGTGGCTGCCGGGGGAGCGCATTCGCAATGGGGAAGAGTGGAT 660  
Db 601 GAGACACATCGCTGGTGGCTGCCGGGGGAGCGCATTCGCAATGGGGAAGAGTGGAT 660  
QY 661 GTACCCATCAAGCTCTACTGTAAAGGGGACGCGAGTGGCTGGTCCCATTCGCGCTGC 720  
Db 661 GTACCCATCAAGCTCTACTGTAAAGGGGACGCGAGTGGCTGGTCCCATTCGCGCTGC 720  
QY 721 ATGTGCAAGAGCGCTTCCGAGGCGGTGAGAAATGGACCGTCTCCGAGTGTTCATCT 780  
Db 721 ATGTGCAAGAGCGCTTCCGAGGCGGTGAGAAATGGACCGTCTCCGAGTGTTCATCT 780  
QY 781 GGGACTTTCAAGGGCAACAAAGGGATGAGGCGTGTACCCACTGTCCATCAACAGCGG 840  
Db 781 GGGACTTTCAAGGGCAACAAAGGGATGAGGCGTGTACCCACTGTCCATCAACAGCGG 840  
QY 841 ACCACTTCTGAAGGGGCGCACCAACTGTGTCTGCGCAATGGCTACTACAGAGACCTG 900  
Db 841 ACCACTTCTGAAGGGGCGCACCAACTGTGTCTGCGCAATGGCTACTACAGAGACCTG 900  
QY 901 GACCCCTGAGACATGCGCTGACAAACATCCCTCCGCGCGCCGAGGTGTGATTTCCAGT 960  
Db 901 GACCCCTGAGACATGCGCTGACAAACATCCCTCCGCGCGCCGAGGTGTGATTTCCAGT 960  
QY 961 GTCAATGAGACCTTCCATGCTGAGTGGACCCCTCCGCGAGCTCGGAGGCGGAGAG 1020  
Db 961 GTCAATGAGACCTTCCATGCTGAGTGGACCCCTCCGCGAGCTCGGAGGCGGAGAG 1020  
QY 1021 GACCTGTCTAACAATCATCTGCAAGAGCTGTGGGCGGGGTCCTGACCCGC 1080  
Db 1021 GACCTGTCTAACAATCATCTGCAAGAGCTGTGGGCGGGGTCCTGACCCGC 1080  
QY 1081 TGGCGGAGCAATGTACAGTACGACGACACGCAAGCTTACGCTGACCGACGCAATTAC 1140  
Db 1081 TGGCGGAGCAATGTACAGTACGACGACACGCAAGCTTACGCTGACCGACGCAATTAC 1140  
QY 1141 ATCAGTACCTGTGGGCGCCACACCACTTACACTTTCAGATCCAGGCTGTGAAGGGCTT 1200  
Db 1141 ATCAGTACCTGTGGGCGCCACACCACTTACACTTTCAGATCCAGGCTGTGAAGGGCTT 1200  
QY 1201 ACTGACCAAGAGCCCTTCTGCGCTCAAGTTGCTGTGAACATCACCAACCAAGGCA 1260  
Db 1201 ACTGACCAAGAGCCCTTCTGCGCTCAAGTTGCTGTGAACATCACCAACCAAGGCA 1260  
QY 1261 GCTCCATGCGGAGTGTCAATCATGATGAGTGGGCGGCAACCGTGGACAGATTAACCTG 1320  
Db 1261 GCTCCATGCGGAGTGTCAATCATGATGAGTGGGCGGCAACCGTGGACAGATTAACCTG 1320  
QY 1321 TCGTGTTCACAGCGGACAGCCCAATGGGCTGATCTCTGCACTGTGAGCTGCACTAT 1380  
Db 1321 TCGTGTTCACAGCGGACAGCCCAATGGGCTGATCTCTGCACTGTGAGCTGCACTAT 1380  
QY 1381 GAGAGGAGCTCACTGTAGTCAACAGCCACACCACTTAAGAGCCCAACAGCGGTACG 1440  
Db 1381 GAGAGGAGCTCACTGTAGTCAACAGCCACACCACTTAAGAGCCCAACAGCGGTACG 1440  
QY 1441 GGCCTCAAGCGCGGCGCATCTATGTCTTCCAGGTGGGCGAGCACTGTGGCAGGCTAC 1500  
Db 1441 GGCCTCAAGCGCGGCGCATCTATGTCTTCCAGGTGGGCGAGCACTGTGGCAGGCTAC 1500

Db 1441 GGCCTCAAGCCGGCCGACATATGCTTTCAGAGTGGGGACGACATGTGGCAGGCTAC 1500  
QY 1501 GGGCGCTAAGGGGGGAAGTACTTCCAGACATAGAGAAAGCCAGTACCAAGACAAGC 1560  
Db 1501 GGGCGCTAAGGGGGGAAGTACTTCCAGACATAGAGAAAGCCAGTACCAAGACAAGC 1560  
QY 1561 ATCCAGGAGAAGTGGGACATCATCGGCTCCGGCGCTGGGCTGGCTCTCCATTT 1620  
Db 1561 ATCCAGGAGAAGTGGGACATCATCGGCTCCGGCGCTGGGCTGGCTCTCCATTT 1620  
QY 1621 GGTGGTGTGATCGCATCGTGTGTAAACAGAGGGGGTTGAGCGTGTGACTCGAG 1680  
Db 1621 GGTGGTGTGATCGCATCGTGTGTAAACAGAGGGGGTTGAGCGTGTGACTCGAG 1680  
QY 1681 TACACGGAAGGTGCAACACTACACAGTGGGACATTAACCCAGGCAATGAAGATCTAC 1740  
Db 1681 TACACGGAAGGTGCAACACTACACAGTGGGACATTAACCCAGGCAATGAAGATCTAC 1740  
QY 1741 ATCGATCTTTCACCTACGAGAGACCCCAAGAGGAGTGGGAGTTCGCAAGAAATT 1800  
Db 1741 ATCGATCTTTCACCTACGAGAGACCCCAAGAGGAGTGGGAGTTCGCAAGAAATT 1800  
QY 1801 GACATCTCTGTGTCAAAATTGAGAGGTATCGAGAGGAGGAGTGGGAGGCTGTGC 1860  
Db 1801 GACATCTCTGTGTCAAAATTGAGAGGTATCGAGAGGAGGAGTGGGAGGCTGTGC 1860  
QY 1861 AGTGGCCACTTGAAGTGGCAGGAGAGAGAGATCTTTGTGGCCATCAAGAGCTCAAG 1920  
Db 1861 AGTGGCCACTTGAAGTGGCAGGAGAGAGAGATCTTTGTGGCCATCAAGAGCTCAAG 1920  
QY 1921 TCGGGCTACAGGAGAGAGAGCGCGGACTTCTGAGCGAAGCTTCATCATGAGCCAG 1980  
Db 1921 TCGGGCTACAGGAGAGAGAGCGCGGACTTCTGAGCGAAGCTTCATCATGAGCCAG 1980  
QY 1981 TTGAGCCATCCCAAGCTATCCACCTGAGAGGTGTCTGACCAAGAGCACCTGTGATG 2040  
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QY 2041 ATCATACCGAGTTCATGAGAGATGGCTCCCTGAGACTCTTCTCCGGCAAAAGATGGG 2100  
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Db 2101 CAGTTACAGATCATCCAGCTGATCCACCTGAGAGGTGTCTGACCAAGAGCACCTGTGATG 2160  
QY 2161 CTGGCAGACATGAACTATGTTCACCTGAGCTGGCTGCCCAACATCTCTCAACAGC 2220  
Db 2161 CTGGCAGACATGAACTATGTTCACCTGAGCTGGCTGCCCAACATCTCTCAACAGC 2220  
QY 2221 AACCTGGTCCGAAAGTGTGCGACTTGGGCTGCTACGCTTCTAGAGAGCATACCTCA 2280  
Db 2221 AACCTGGTCCGAAAGTGTGCGACTTGGGCTGCTACGCTTCTAGAGAGCATACCTCA 2280  
QY 2281 GACCCCACTACACAGCTGCTGGGCGGAAAGTTCCCATCCGCTGAGAGCCCGGAA 2340  
Db 2281 GACCCCACTACACAGCTGCTGGGCGGAAAGTTCCCATCCGCTGAGAGCCCGGAA 2340  
QY 2341 GCCATCCAGTACCGGAGTTCACTTGGCCAGTGTGTGAGGACTACGCGCATTTGCATG 2400  
Db 2341 GCCATCCAGTACCGGAGTTCACTTGGCCAGTGTGTGAGGACTACGCGCATTTGCATG 2400  
QY 2401 TGGGAGGTATGCTATGAGGGGAGGGGCTACTGGGACATGACCAACAGATGTAAATC 2460  
Db 2401 TGGGAGGTATGCTATGAGGGGAGGGGCTACTGGGACATGACCAACAGATGTAAATC 2460  
QY 2461 AATGCCATTGAGAGGACTATCGGCTGCCACCGCCATGGATGGAGCGCCCTGCAAC 2520  
Db 2461 AATGCCATTGAGAGGACTATCGGCTGCCACCGCCATGGATGGAGCGCCCTGCAAC 2520  
QY 2521 CAACATGCTGAGCTGTTGGCAGAAAGACCGCAACCGGCGCAAGTTGGCGCAAAATT 2580  
Db 2521 CAACATGCTGAGCTGTTGGCAGAAAGACCGCAACCGGCGCAAGTTGGCGCAAAATT 2580

QY 2581 GTCAACACGCTAGACAAGATGATCCGAATCCCAACAGCCTCAAAAGCATGGGCGCTTC 2640  
Db 2581 GTCAACACGCTAGACAAGATGATCCGAATCCCAACAGCCTCAAAAGCATGGGCGCTTC 2640  
QY 2641 TCCTTGGCATCAACCTGCGCTGTGTGAACCGCAGCATCCCGCATCAACCAAGCTTTAAC 2700  
Db 2641 TCCTTGGCATCAACCTGCGCTGTGTGAACCGCAGCATCCCGCATCAACCAAGCTTTAAC 2700  
QY 2701 ACGGTGAGAGAGTGGCTGAGAGGCTATCAAGATGGGCGATACAAAGAGAGCTTCGCAAT 2760  
Db 2701 ACGGTGAGAGAGTGGCTGAGAGGCTATCAAGATGGGCGATACAAAGAGAGCTTCGCAAT 2760  
QY 2761 GCGGCTTCACTCTTTGACAGTGTGTCTGACATGATGAGAGACAATTCGCGGTT 2820  
Db 2761 GCGGCTTCACTCTTTGACAGTGTGTCTGACATGATGAGAGACAATTCGCGGTT 2820  
QY 2821 GGGGTCACTTTGGCTGGGCGCACAGAAAAAATCTGAACAGTATCCAGGTGATGGGCGG 2880  
Db 2821 GGGGTCACTTTGGCTGGGCGCACAGAAAAAATCTGAACAGTATCCAGGTGATGGGCGG 2880  
QY 2881 CAGATCAACCAATGATGTGTGAGAGTTTGACATTCACTGCTCGGCTCACTCTTC 2940  
Db 2881 CAGATCAACCAATGATGTGTGAGAGTTTGACATTCACTGCTCGGCTCACTCTTC 2940  
QY 2941 CTCCAGCCCCCGCCCTCTGC 2962  
Db 2941 CTCCAGCCCCCGCCCTCTGC 2962

RESULT 4  
US-08-542-635-1  
; Sequence 1, Application: US/08542635  
; Patent No. 6218356  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeier, Mark  
; APPLICANT: Letwin, Kenneth  
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
; TITLE OF INVENTION: TYROSINE KINASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bereskin & Parr  
; STREET: 40 King Street West, Box 401  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,635  
; FILING DATE:  
; CLASSIFICATION: E00  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mediamid, Shona S.  
; REGISTRATION NUMBER: 38,798  
; REFERENCE/DOCKET NUMBER: 3153-162  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 364-1398  
; TELEX: 06-23115  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3105 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:

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: ORGANISM: Mus musculus
: DEVELOPMENTAL STAGE: Embryo
: IMMEDIATE SOURCE:
: LIBRARY: Lambda gt10 cDNA library
: CLONE: Combined PnukRACE A2 and K2 AND cDNA clones
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: Distal end of chromosome 4
: MAP POSITION: near the and-1 mutation
: US-08-542-635-1

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Query Match      84.3%  Score 2498;  DB 4;  Length 3105;
Best Local Similarity 90.5%;  Pred. No. 0;
Matches 2679;  Conservative 0;  Mismatches 275;  Indels 6;  Gaps 1;

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QY 1 CTGCTCCCGCCGCTGGAAGAAACGCTAATGACTCCACTACAGCACTGCTGAGTGGGC 60
DB 67 CTCTAGACCCCGCTGGAGAAACCTGATGAGACTTACAGCAAGCAAGGCTGAGCTGGGC 126
QY 61 TGGATGGTGCATCTCCATCAGAGTGGGAGAGAGTGAAGTGGCTAGCATGAAACATGAAC 120
DB 127 TGGATGGTGCATCTCCATCAGAGTGGGAGAGAGTGAAGTGGCTAGCATGAAACATGAAC 186
QY 121 AGCATCCGACAGTACCAGGTGTGCAACGTGTTGAGTCAAGCCAGAACTGGCTAGC 180
DB 187 ACTATCCGATCCTACAGAGGTGTGCAACGTGTTGAGTCAAGCCAGAACTGGCTAGC 246
QY 181 ACCAATTTATCCGGGCGGCTGGGCGCCACCCGATCCACGTGAGAGTGAAGTTTGGGTG 240
DB 247 ACCAATTTATCCGGGCGGCTGGGCGCCACCCGATCCACGTGAGAGTGAAGTTTGGGTG 306
QY 241 CGTACTGACAGAGCATATCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 307 CGTACTGACAGAGCATATCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
QY 301 TACTATGAGAGCTGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 367 TACTATGAGAGCTGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
QY 361 TGGGTGAAGGTGATACCATTCGACCGGACGAGAGTCTTCCAGTGGAGTGGAGTGGC 420
DB 427 TGGGTGAAGGTGATACCATTCGACCGGACGAGAGTCTTCCAGTGGAGTGGAGTGGC 486
QY 421 CGCGTATGAAATCAACACGAGTGGGAGCTTGGAGTGGTGGTGGTGGTGGTGGTGGTGG 480
DB 487 CGCGTATGAAATCAACACGAGTGGGAGCTTGGAGTGGTGGTGGTGGTGGTGGTGGTGG 546
QY 481 TACCTGGCTTCCAGAGTATGAGGCTGATGCTCCATCGCCGCTGCTGCTTCTAC 540
DB 547 TACCTGGCTTCCAGAGTATGAGGCTGATGCTCCATCGCCGCTGCTGCTTCTAC 606
QY 541 CGCAGTCCCGCCGATCATCCAGAAATGGGCGCATCTTCCAGAAACCTCTGCGGGGCT 600
DB 607 CGCAGTCCCGCCGATCATCCAGAAATGGGCGCATCTTCCAGAAACCTCTGCGGGGCT 666
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DB 667 GAGAGCATATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
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DB 727 GTACCCATCAAGCTCTACTGTAAGAGGAGGAGCGGAGTGGCTGAGTGGCTGAGTGGCTGAG 786
QY 721 ATGTGCAAGAGGCTTCCAGAGGCTTGAAGATGGCAACGCTGCGAGGTTGGCTATCT 780
DB 787 ATGTGCAAGAGGCTTCCAGAGGCTTGAAGATGGCAACGCTGCGAGGTTGGCTATCT 846
QY 781 GGGACTTTCAAGGCAACCAAGGAGTGAAGGCTTCAACCACTGCTCCATCAACAGCGG 840
DB 847 GGAACCTTCAAGGCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 906
QY 841 ACCACTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900

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DB 907 ACCACTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 966
QY 901 GACCCCTTGAAGATGCTGCAACCAATCCCTTCCGCGGCGGCGGCGGCGGCGGCGGCGG 960
DB 967 GACCCCTTGAAGATGCTGCAACCAATCCCTTCCGCGGCGGCGGCGGCGGCGGCGGCGG 1026
QY 961 GTCATGAGAGCTTCCCTCATGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
DB 1027 GTCATGAGAGCTTCCCTCATGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1086
QY 1021 GACTCTGCTACACATCATCTGCAAGAGCTGTGGCTGGGCGGCGGCGGCGGCGGCGGCGG 1080
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QY 1141 ATCAATGAGCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
DB 1207 ATCAATGAGCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1266
QY 1201 ACTGACCAAGAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1267 ACTGACCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 1261 GCTCATGCGGAGTGTCCATCATGATGAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320
DB 1327 GCTCATGCGGAGTGTCCATCATGATGAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1386
QY 1321 TCGTGTGCTCCAGCGGAGCAAGCCCAATGCGTGAATCTGAGTATGAGTATGAGTAT 1380
DB 1387 TCGTGTGCTCCAGCGGAGCAAGCCCAATGCGTGAATCTGAGTATGAGTATGAGTAT 1446
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QY 1440 -----GGGCGCTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1494
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DB 1567 GGCATGAGGCGGCTCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1626
QY 1555 ACAAGCATCCAGAGGAGGAGTGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1614
DB 1627 ACAAGCATCCAGAGGAGGAGTGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
QY 1615 CTCATGCTGTGGTGTATCATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1674
DB 1687 CTCATGCTGTGGTGTATCATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1746
QY 1675 TGGAGTATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1734
DB 1747 TCGAGTATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1806
QY 1735 ATCTACATGATCTCTTCACTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1794
DB 1807 ATCTACATGATCTCTTCACTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1866
QY 1795 GAAATTTGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854
DB 1867 GAAATTTGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1926
QY 1855 GTCTGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1914
DB 1927 GTCTGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1986
QY 1915 CTCAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1974
DB 1987 CTCAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2046

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QY 1975 GGCACATTGACCATTCACAGCTGAGGGGTCTGTGACCAAGACACACT 2034
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Db 2047 GGCACATTGACCATTCACAGCTGAGGGGTCTGTGACCAAGACACACT 2106
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Db 2107 GTCATATCATCATCACTGAATTCATGAGAAATGAGTCTGAGCTCTTCTCCGGCAAAAT 2166
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QY 2095 GATGGCAGTTCACATCATCACTGAGTGGGGCATGCTCCGGGCAATCCAGCTGGCATG 2154
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QY 2155 AAGTACCTGGCAGACATGAACTATGTTACACCTGACCTGCTCCCGCAACATCTCTGTC 2214
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Db 2227 AAGTACCTGGCAGACATGAACTATGTTACACCTGACCTGCTCCCGCAACATCTCTGTC 2286
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QY 2275 ACCGACAGACCCACCTACACAGCTGCTGGGGGAAAGTTCCCAATCCGCTGGACAGCC 2334
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QY 2335 CCGGAAAGCCTCAGTACCGGAAAGTCCCTGCGCCAGTATGTGTGAGCTACGCGCAT 2394
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QY 2395 GTATGATGGAGGTGATGCTCTATGGGGAGCGGGCCCTACTGGGACATGACCAACAGAT 2454
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QY 2515 CTGACCAACATCATGCTGAGCTGTTGGCAAGAGGACCGCAACCGGGCCCAATGTTGGC 2574
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QY 2575 CAATGTCACACGCTAGACAGATGATCCGCAATCCCAACAGCTCAAAAGCCATGGCG 2634
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QY 2635 CCCCTCTCTGTGCAATCACTGCGCTGTGAGACCGCAAGATCCCGGCTACACAGC 2694
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Db 2707 CCCCTCTCTGTGCAATCACTGCGCTGTGAGACCGCAAGATCCCGGCTACACAGC 2766
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QY 2815 CGGGTGGGGGTACATTGGCTGGGGCCACCAAGAAAAATCTGAACAGATCAGTGTATG 2874
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Db 2887 CGGGTGGGGGTACATTGGCTGGGGCCACCAAGAAAAATCTGAACAGATCAGTGTATG 2946
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QY 2875 CGGGGCGAGATGAAACAGATTCAGTGTGAGAGTTTGACATTCCTGCTCGGCTAC 2934
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QY 2935 CTCCTCTCTCAAGCCCGCC 2954
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RESULT 5  
US-08-162-809-17  
; Sequence 17, Application US/08162809

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; Patent No. 5457048
; GENERAL INFORMATION:
; APPLICANT: pasquale, Elena B.
; APPLICANT: sajjadi, Fereydoon G.
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4049 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..2994
; US-08-162-809-17

Query Match 73.8%; Score 2185.6; DB 1; Length 4049;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 464; Indels 9; Gaps 2;

QY 1 CTGCTGCGCGCGCTGGAAGAAAGCTAATGAGCTCCACTACAGCCACTGCTGAGCTGGGC 60
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Db 76 CTGCTGCGCGCGCTGGAAGAAAGCTAATGAGCTCCACTACAGCCACTGCTGAGCTGGGC 135
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QY 61 TGGATGCTGATCTCTCATCAGAGGTGGGAAAGAGTGAAGTGGCTACGATGAGAAATGAAAC 120
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Db 136 TGGATGCTGATCTCTCATCAGAGGTGGGAAAGAGTGAAGTGGCTACGATGAGAAATGAAAC 195
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QY 121 ACGATCCGACAGTACAGAGTGTGCAACGTTTGAAGTCAAGCCAGAAACAATGCTGACG 180
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Db 196 ACGATCCGACAGTACAGAGTGTGCAACGTTTGAAGTCAAGCCAGAAACAATGCTGACG 255
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QY 181 ACCAAGTTTATCCGCGCGCTGGGGCCCAACGATCCAGTCCAGTGGAGATTTTGGGTG 240
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Db 256 ACCAAGTTTATCCGCGCGCGCTGGGGCCCAACGATCCAGTCCAGTGGAGATTTTGGGTG 315
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QY 241 CGTACAGCAGCAGTACCCAGAGTCTGAGCTCTGCAAGAGAGACCTTCAACCTCTAT 300
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Db 316 CGGAGTGGACAGCAGTACCCCAAGCTCCCGGGCTCTGTAAGAGACTTTTAACTCTAT 375
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QY 301 TACTATGAGGCTGACTTGTGACTGGGCCACCAAGACCTTCCCAATGAGTGGAGATCCA 360
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Db 376 TACTATGAGGCTGACTTGTGACTGGGCCACCAAGACCTTCCCAATGAGTGGAGATCCA 435
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QY 361 TGGGTGAAGGTGATACCATTTGACGAGCGAGAGAGCTTCTCCAGTGTGAGTGGTGGC 420
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Db 436 TGGGTGAAGGTGATACCATTTGACGAGCGAGAGAGCTTCTCCAGTGTGAGTGGTGGC 495
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OY	421	CGCGTCATGAAATATCAACACCGAGAGTGGAGAGCTTGGAGACTGTGTCCGACCGGCTTC	480
Db	496	CGGGATGATGAAGATTAAACACGAGAGTGGCGAGTTTGTGGGCTGTCTCCAAAAACGGTTTAC	555
OY	481	TACCTGGCCTTTCAGAGCATATGAGCGCGGCATGTCCCTCATGCGCGGTGTCTCTAC	540
Db	556	TACCTGGCCTTTCAGAGCATATGAGCGCGGTGTCTCTCATGATTCAGTCCGTGTCTTTTAC	615
OY	541	CGCAAGTCCCGCCCGCATTCACAGATGGCGCATCTTTCAGGAAACCCCTGTCCGGGGCT	600
Db	616	CGCAAGTCTCCCGGTGTATCAAAAGGGGGCGGTCTTTCAGGAAACCCCTGTCCGGAGCG	675
OY	601	GAGACACATCGCTGTGTGGTGGCCCGGGGGAGCGCATATGCCCAATCGGAAGAGTGTAT	660
Db	676	GAGACACATCTCTGTGTGGCAGCCCGGGGGAGCGTCATCAGCAATCGGAGAGGTGTGAT	735
OY	661	GTACCCATCAAGCTCTACTGTACGGGGAGCGGCGAGTGGTGGTCCCATTCGGGCGCTTC	720
Db	736	GTGCCCATCAAGCTGTACTGTCAATGTGGGAGTGGCGAGTGGTGGTCCCATTCGGGCGCTTC	795
OY	721	ATGTCAAAAGCAGCTTTCGAGGCGCTTGTAGATGGCACCGTCTGTCCGAGGTGTCCATCT	780
Db	796	ATGTCTCAGCGCGGCTTAAGATCTCGTGTGAAATGTGGACCTGTCTGACAGAGGTGCCATCA	855
OY	781	GGAGTTTCAAGGGCAACCAAGGGGAGTGAAGGCGTGTATCCACAGTGTCCCATCAACAGCCGG	840
Db	856	GGAGCTTCAAGGGCAGCAAGGAGATGAAGATGTCTCATTTGTCCATTAATCAACCCGG	915
OY	841	ACCACTTCTGAAGGGGCGCACCAACTGTGTCTGGCGCATGTGGCTACTACAGAGACACTGTG	900
Db	916	ACGACTTCTGAAGGGGCGCACCAACTGTGTGTGGCGAAAGGAGATTAACCGGAGATGTCT	975
OY	901	GACCCCTGTGACATGTCCCTGTGACACCACTCCCTCCGCGCCCGCCAGGCTGTATTTCAGT	960
Db	976	GACCCCTGTGACATGTCCCTGTGACACCACTCCCTCCGCGCCCGCCAGGCTGTATTTCAGC	1035
OY	961	GTCAATGAGACCTCCCTCATGTGTGGATGGAGACCCCTCCCGCGCATCTCGGAAGGCGAGAG	1020
Db	1036	GTGAATGAACCTCCCTCATGTGTGGATGGAGACCCCTCCCGCGCATCTCGGAAGGCGGAG	1095
OY	1021	GACCTGTCTAACATCATCTGTGCAGAGCTGTGGCTCGGGCCGGGGTGCCTGCACACCCGC	1080
Db	1096	GATCTGTGTATCAACATCATCTGTGCAGAGCTGTGGGTCAGAGCGCTGTGGGCTGTGCACGCGC	1155
OY	1081	TGCGGGGACATGTACAGTACGACACACCGCCACTTGGCTGTACCGACGCGACGATTTAC	1140
Db	1156	TGTGGGGCAACGTGACAGTTTGGCCCCACGGCACTGGGCTGTGCGAGGCTGTGCATCTAC	1215
OY	1141	ATCAGTGCACGTGTGGGCCACACCCAGCAATACCTTGGAGTCCAGGCTGTGAAGCGCGTT	1200
Db	1216	ATCAGGCAACGTGTGGGCCACACCGCACTTACCTTTGAGATTCAGGCTGTGAATGGGTTC	1275
OY	1201	ACTGACAGAGCCCCCTTCTGCGCTCAGTTTCGCTGTGAAATCAACCAACAGGCA	1260
Db	1276	ACCGCAGAGCCCCCTTCTCCCAAGTTTGCATCAGTAAATATCACCAACACGAGCT	1335
OY	1261	GCTCATATGGGAGTGTCCATCATATGACATCAGGTGAGCGGCAACCGTGTGACAGCATTTACCTG	1320
Db	1336	GCTCATATAGCCGTTGTCCATTAATGACACCAAGTGTAGCGCACTGTGACAGCATTTACCTTC	1395
OY	1321	TCTGTGTCCACGCGGACGACGCCCAATGTGGTGTATCTGTGATATGAGTGTGCAATATAT	1380
Db	1396	TCTGTGTCTCAACCTGTACGACGCCCAATGTGATCTCTGTGATTTATGAGTGTGCAATATAT	1455
OY	1381	GAGAAAGAGCTCAGTGTAGTCAACAGCCACAGCCATTAATAAGCCCAACCAACGCTCACG	1440
Db	1456	GAGAAAGAACTCAGTGTAGTAAATTAATCAACAGCAAGTGAAGAGCCCAACCAACTGTGACA	1515
OY	1441	G-----GCCCTAAAGCGCGCGCATCTATGTCTTCAGAGTGGGGGCAAGCACTGTGGCA	1490
Db	1516	GTGCAAAACCTCAAAAGCTGGCACCACTATGTCTTCTCAAGTGGGAGCAAGTACCGTGGCT	1575

QY	1495	GCTTAGGGGGGCTACAGCGGCAAGATGTACTTCCAAACCATGACAGAAACCGAGTACCAAG	1554
Db	1576	GGGTATATGGCCGGATATGATGGCAAGATGTACTTCCAAACCATGATGTAAACCGGATCTCCAG	1635
QY	1555	ACAGACATCCAGGAGAAGTTGGCCACTCATCATGAGGTCCGCGGCGCTGAGCCGTGGCTTC	1614
Db	1636	ACCAAGTGTCCAGGAGAAGCTGCCACTCATCATTTGGCTCCTCTGACGACGAGTGGTGT	1695
QY	1615	CTCATGTCTGTGGTTGTTCATCGGCATCGTGTGTAC - - AGAGCGGGGTTTGAAGCTGCT	1671
Db	1696	CTCATGTCTGTGTCTCATCATTTATTTGTCCTGCACAGAAAGACGGGGCTTTGAAACGTGCT	1755
QY	1672	GACTCGGAGTACACGGGACAAAGCTGCAACACTACACAGTGGCCACATTAACCCAGGCATG	1731
Db	1756	GACTGTGAGTACACTACAAAGCTGCAGCACTATACCAAGTGGCCACTCTCCAGGGAATG	1815
QY	1732	AAGATTACATCATCTCTTTCACCTACAGAGACCCCAACAGGACATGTGGGGAGTTTGGC	1791
Db	1816	AAGATTATATCATCATCTTACTTACCTACGAAGATCCCAATAGAGCTGTCAAGGAAITTTGCA	1875
QY	1792	AAGAAATTTGACATCTCTGTGTCAAAATTTGAGCAGTATCGGACAGGGAGTTTGGC	1851
Db	1876	AAGAATTTGATATCTCTGTGTGAAATTCAGACAGTATTTGGGCAAGGGAGTTTGGT	1935
QY	1852	GAGGTCTGACAGTGGCCACTGAAGCTGCCAGGCAAGAGAGATCTTTTGGCCATCAAG	1911
Db	1936	GAGGTGTGACAGTGGGCTCTCAAGCTTCTCGGCAAAAGAGATCTTTTGGCCATCAAG	1995
QY	1912	AGCCTACAGTGGGGCTACACGGGAAGACGGCGGGCACTTCTGTAGCGCAACCTCCATC	1971
Db	1996	ACCTTCAAGCTGTGGTTACACAGGAAGACAGACGGGACTTCTGTAGTAAACCCAGCACTC	2055
QY	1972	ATGGGCGCACTTGGACCATCCCAACGTCATCCACCTTGGAGGTGTGCTGACCAAGAGCACA	2031
Db	2056	ATGGGCGCACTTTGACCAACCCCAATGTCTATCCACCTGGAAGGGGTGTGACCAAGATTTCC	2115
QY	2032	CCTGTGATGATCATCACCGAGTTTCATGAGAAATGGCTCCCTGGACTCTTTTCCGGCAA	2091
Db	2116	CCAGTCTATGATCATTTACAGAGTTTCATGAGAAATGGCTCTTGGACTCTTTTGAAGGCAA	2175
QY	2092	AAGCATGGGCGAGTTCACACTTCATCCACGCTGGTGGGATATGCTTCCGGGCAATCGCACTGGC	2151
Db	2176	AATGATGGGCGAGTTTCAACATGTATCCACGCTGGGCGATTTCTGTGGCACTTTCACACAGGC	2235
QY	2152	ATGAAGTACTTGGGACAGACTGAAGACTATGTTCACCGTACCTGGCTGGCCGCAAACTCCGC	2211
Db	2236	ATGAAGTACTTGGGCTGATATGTGAACATACGTGACACCGGACCTGGCTGCCGCAAACTCTCG	2295
QY	2212	GTCAACAGCAACCTGGTCTGCAAGGTGTGCAACTTTTGGGCTCTCAACGCTTCTTAGAGNAC	2271
Db	2296	GTCAACAGCAACCTGGTCTGCAAGGTGTGCAAGGTGTGCAAGGTGTGCAAGGTGTGCAAGGT	2355
QY	2272	GATACTCTGACACCCCACTACACACAGTGGCCCTTGGGCGGAAAGTTCCCATTCGCTGGACA	2331
Db	2356	GACACTCTGATCCCACTTACACACAGCGCACTGGGTGGAAGATCCCAATACGGGTGGACA	2415
QY	2332	GGCCGGGAAGCCATCCAGTACCGGGAATTTACCTGGGCGAGTATGTGGAGTCATACGGC	2391
Db	2416	GGCGCTGAGGCAATTCAGTACCGGAAATTTACATACAGCCAGGATGTGTGGAGCTATGGA	2475
QY	2392	ATTGTCTATGTGGAGGTGATGTCTTATGGGGAAGCGGCCCTTACTTGGACATGTACCAACAG	2451
Db	2476	ATATGTCATGTGGAGGTGATGTGTGTACGGCGAGGGCCCTTACTTGGACATGTACCAATCA	2535
QY	2452	GATGTATATCATTCATTTGACGAGACTATGTGGCTGCCACGGCCCATGAGACTGCCGAGC	2511
Db	2536	GATGTATATTAATGCTATTTGAGCAGGACTATCGGCTACCAACCCCTATGATTTGTCCAAT	2595
QY	2512	GGCCGGAACCACTATCTGTGACGTGGTGGCAAGAGACCCGCAACACCGGCGCCCAAGTTC	2571
Db	2596	GGCCCTGACCAACTATGTCTGTAGCTGTGGCGAAGAGATTCGAACCAACAGACCAAAATTT	2655
QY	2572	GGCCAAATTTGTCAACAGCTATGACAAAGATGTATCCGAATCCCAACAGCCTCAAAAGCCATG	2631



Db	2656	GGACAGATTGTCAACACTTTAGCAAAATGATCCGAATTCCTAATATGCTGAAGCCATG	271.5
QY	2632	GGGCCCCCTCTCTCTGTGGCATCAACTGCGCGTGTGTGGACCGCAGCATGCCCGACTACACC	265.1
Db	2716	GCACCTCTCCCTCTGGGGTTAACTCCCTCTACTTGACCGGCACATCCAGATTTATACC	277.5
QY	2692	AGCTTTAACACGGTGGAGCGATGGCTGGAGGCGATCAAGATGGGCGAGTAAAGAGAGC	275.1
Db	2776	AGCTTACACACTGTGGATGTAATGGCTGTGGATGCCATCCAGATAGCCATACAGAGAGAC	283.5
QY	2752	TTGCGCAATGCCGCGTTCACTCTCTTTGACGTGTGTCTCAGATGATGAGAGACATT	281.1
Db	2836	TTTCCACGTCTGGCTTACACACTTTGATATGATATCTCAATGACGTGTGAGAGACATT	289.5
QY	2812	CTCCGGGTTGGGGTCACTTGGTGTGGCCACCGAAAAAATCCGTACAGATCCAGTG	287.1
Db	2896	CTACGAATTTGGGGTCACTTTAGCAGAGACACCGAAGAAATTTCTAACAAGTATCCAGGTG	295.5
QY	2872	ATGCGGGCGAGATGTAACACAGATTCAGTGTGTGGAGTTTGAATTCACCTGCCCTGGCT	293.1
Db	2956	ATGAGACACAGATGAACCAAAATTCAGTCTGTGGAGTTTGAATTCACACAGCTCCTGTG	301.5
QY	2932	CACCTTTCTCCAAAGCCCCCGCCCC	295.7
Db	3016	CTCCACTTCTCTAGAGCCCTGCTGCC	304.1

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Query Match	71.8%;	Score 2127.6;	DB 1;	Length 4097;
Best Local Similarity	82.7%;	Pred. No. 0;		
Matches 2493;	Conservative	0;	Mismatches 464;	Indels 57;
				Gaps 3

QY	1	CTGTGCGCCCGCTGGAAACACGGCTAAATGAGACTCTCACTACAGGACACTGCTGACCTGGC	80
Db	76	CTGTGCGCCCGCTGGAAAGACGCTGATGAGACTCTCAACAGCGCCACAGCAGACTGGGC	135
QY	61	TGCGATGTGCATCTCTCCATCAGGGTGGGAAAGGTGAGTGGCTACGATGAAACATGAA	120
Db	136	TGGATGGTGTATCTCTCCCTCAGGTGGGAAAGGTGAGTGGCTATTCGATGAAACATGAA	195
QY	121	ACGATCGCACGACGATCAGGTGTGCAACGTTTGATGAGTCAAGCCAGAACATCTGGCTACGG	180
Db	196	ACCATCGCACCTACCAAGGTGTGCMAACGTTTGAATCCAGCAAAACATCTGGCTCGG	255
QY	181	ACCAAGTTTATCCGCGCCCGTGGGCCACCCGATCACCAGTGGAGATGAATTTTGGGTG	240
Db	256	ACCAAGTATCTCCGAGGGGAGGAGCGCACCCGATCCACGTGGAGATGAATTTCTCGTT	315
QY	241	CGTGACTGCGACGACGATCCGACGCGTGGCTCTCGTCAAGGAGAACCTTCAACCTCTAT	300
Db	316	CGGAGACTGCGACGACATCCCAACGTCGCGGCTCTCTGAAGAGACTTTTAACCTCTAT	375
QY	301	TACTATGAGGCTACTTTTGACTCGGCCACCAAGACCTTTCCCACTGGATGGAGATCA	360
Db	376	TACTAGCAATCAGACTTTTGACTCTGCCACCAAGACTTTTCTTAATGATGAAACACCT	435
QY	361	TGGGTGAAGTGGATACCATTTGACGCCGACGAGACTTCTCCAGAGTGGACCTGGGTGGC	420
Db	436	TGGATGAAGGTAAATACAAATGCTGCGCAGAGAGACTTCTCGAGAGTGGACCTTGGTGGG	495
QY	421	CGGCTATGAAATCAACACCGAGGTGCGAGACTTCTCGACACTGTGTCCCGACGCGCTTC	480
Db	496	CGGCTATGAAATTAACACCGAGGTGCGACACTTTTGGGCCCTGTCTCCAAACAGGTTTC	555
QY	481	TACCTGGCTCTTCAGAGCATATGGCGGCTGCATGTCCCTCATCGCCGTGCTCTTCTAC	540
Db	556	TACCTGGCTCTTCAGAGCATACGGGGGCTCATGTCTCTGATTTGACGTCGTCGTTTATC	615
QY	541	CGCAAGTGGCCCGCATCATTCGAGATGGCGCATCTTCACAGAAACCTCTCGGGGGCT	600
Db	616	CGCAAGTGGCCCGTGTGATTCAGAAACGGGGCGGTCTTCACAGAAACCTCTCGGGAGCG	675
QY	601	GAGAGCATATCGTGTGTGTGCTGCCCGGGGACGCTGCATGCCCATAATGCGGAAGAGGTGAT	660
Db	676	GAGAGCATATCTCTGCGTGGGACGCCGGGGGAGCGTGCATCAGCAATGCGAGAGAGGTGAT	735
QY	661	GTACCCATCAAGCTCTACTGTATAACGGGGGACGGCGAGTGGCTGTGCCATGGGGCGCTGC	720
Db	736	GTCGCCCATCAAGCTCTACTGTATGCGAATGGGGGATGCGAATGGCTGTGCCATGGCGGCTGC	795
QY	721	ATGTGCAACAGCAGGCTTCGAGGGCGCTTGTGAATGGCAGCGTGTGCGGAGGTGTTCATCT	780
Db	796	ATGTGCAAGCGCCGGGCTATATGAGTGGGTGGAGAAATGGAGCCGTTGTGCAAGGCTGCCCATCA	855
QY	781	GGGACTTTTCAAGGACCAACCAAGGGGATGAAGCCTGTACCCACTGTGCCATCAACAGCGG	840
Db	856	GGGACTTTTCAAGGGCACCCCAAGGAGATGAAGATGTGTCTATTGTTCATTAACAGCGCGG	915
QY	841	ACCACTTCTGAAGGGGCGCACCAACTGTGTCTGCGCGAATGGCTACTACAGAGCAGACTG	900
Db	916	ACGACTTCTGAAGGGGCGCAGAACTCGTGTGCGCAAAAGGATTAATCCGGGGCGAGATGCT	975
QY	901	GACCCCTCGACATGCCCTGCAACACATCTCCCTCGCGCCCCACAGGCTGTATTTTCAGT	960
Db	976	GACCCCTCGACATGCCATGCAACACCATCTCTGTGCCCCCCACAGGCGGTATCTTCAGC	1035
QY	961	GTCATGAGACTTCCTCATGTGCTGGAATGGAGCCCTTCCCGCGACTCCGAGGCGCGAGAG	1020
Db	1036	GTCATGAAACCTCTCGATGCTGTGAGTGGAGCCCGCACACGAGACTCAAGGGGGCGCGGAG	1095
QY	1021	GACCTGCTTACAACTATCTGTCAAGAGCTGTGGCTCGGGCGGGGGTGTCTGCACCCGC	1080









163 CAGAACACTGGCTACGACCAAGTTATCCGGCGCGTGGGGCCACCCGATCCAGTG 222  
179 CAGAACAACTGGCTTCGCCACCAAGTTATCAGGCCGACAGCGTCCAGCGGTCTAGTG 238  
223 GAGATGAAGTTTTCGGTGGCTGACGACGACATCCCGCGTGGCTCCGTCGAG 282  
239 GAGCTGAATTAATCACTGGCGGAGCTGCACAGCATCCCAACATCCCTGGTCTCGAAA 298  
283 GAGACCTTCAACCTCTTATATAGAGGCTGACTTACCTGGCCACCAAGACTTCC 342  
299 GAGACCTTCAACCTCTTATATAGAGTACAGATACGATTCCTGGCTGCAATAGCCCT 358  
343 AACTGATGAGATCCATGGGTGAAGTGAATGATACATTCGACGCGACGAGAGCTTCC 402  
359 TTCTGATGAGAGAACCCCTTATCAAGATGATATCTGCTCGGATGAGAGCTTCTCC 418  
403 CAGGTGACCTGGGTGGCGCGCTGATGAAAAATCAACACGAGGTGCGGAGCTTGGACT 462  
419 AACTGGAGTCCGGCCG-----TGTAACACCAAGGTTGCGACGCTTGGGCG 466  
463 GTTCCCGCAGCGGCTTCTACCTGGCTTGCAGGACTATGGCGCTCATGTCCCTATC 522  
467 CTCTCCAGATGAGCTTATCTGCTTTCAGAGACCTGGGGGCTGCAATGCTCTATC 526  
523 GCGGTGGTGTCTTCTACCCCAAGTGGCCCGCATCATCCAGATGCGCATCTTCAG 582  
527 TCGGTCCGGGCTTCTTCAAGAAATGTTCCACACCATCGCTGGCTTGTCTATCTCCG 586  
583 GAAACCTGTGGGGGCTGAGACACATGCTGGTGGCTGCCGGGACAGCTGCATGCC 642  
587 GAAACCTTAAGGGGGCTGAGCCACGCTCGTGTATCTGCGCGGACCTGATGCC 646  
643 AATGGGAAGGTGATGATGATCAACATCACTTACTGTAACGGGAGCGGAGTGGCTG 702  
647 AAGCAGTGAATGTCTGTGCTCCCTGAAGCTTACTGCAACGCTGTGCGAGTGATG 706  
703 GTGCCCATCGGGGCTGATGTCMAAGAGCTTGAAGGCTTGAAGGCTGACAGCGTC 762  
707 GTGCTGTGGAGCGTGCAGTGTGCTGTGAGTACGAGCAGCATGAAGATACCCAG 766  
763 TCGCAGAGTTGTCAATCTGGGACTTTCAGAGCCCAACCAAGGGATGAGGCTGTACCAC 822  
767 TGCAGGATGATCGGGCGGAGCTTCAATCCAGAGGAGGAGGCGCTCTCCCTCC 826  
823 TGTCCCATCAACAGCCGAGCACTTCTGAGAGGGGCCAACCACTGTCTCCCAATGGC 882  
827 TGCCTTCCCAACAGCCGACACCGGAGGAGCCAGCTGTGCAATATGTGCAAGCGC 886  
883 TACTACAGAGACCTGAGCCCTGAGCATGCTCCCTCATGCTGGAGTGGACCTCCCGC 942  
887 TTCTTCCGAGCAGCGGAGCCCGCAGACAGGCGCTGCAAGATGTGCTCAGGCCCA 946  
943 CAGGCTGATTTTCAGTGTGATGAGACTCCCTCATGCTGGAGTGGACCTCCCGC 1002  
947 CGCAGCGTATCTTCAACGTGAATGAGAGCTGTGGTGGAGTGGAGCGAGCCAG 1006  
1003 GACTCGGAGGCGGAGAGAGCTGCTACACATCATCATGCAAGAGCTTGGCTGGGCG 1062  
1007 GAGCGGGGGGGGAGATGACTGCTCTACACATCTGCAAGATGAGAGTGCAGCGTGGAG 1066  
1063 CGGGGTGCTGCACCGCTGGGGGCAATGTACAGTACGACACCGCCAGCT----- 1115  
1067 CGCGGCTGTGCGCGCTGGCGACGACAGTGGAGTGTGCGCGGCGCAGTGGGCTC 1126  
1116 --AGGCTTACCGACGACGATTTTACATCAGTGAAGTGTGGCCCAACCCAGTACAC 1173  
1127 ACTGGCTTACTGAGGAGCATCTACATCAGAGTGTATGGCCCAACCCCGTACACC 1186  
1174 TTGAGATCCAGGCTGTGAAGCGCTTACTGACACAGGCGCTTCCGCTCAGTGGCG 1233  
1187 TTGAGATCCAGGCGGTGATGTGATCTCCAGCAAGAGCCCTTACCTCCCACTTTTGGC 1246

1234 TCTGTGAACATCACCAACCAAGCACTCCATCGGCAGTGCTCATCATGATCAGGTG 1293  
1247 TCGCTCAACATCAGACCAACCAAGGAGCCCATCTGCGTGGCCACCATGATCTGCAC 1306  
1294 AGCCGACCGTGGACAGCATTTACCTGTGTGTCCAGGCGGACCAATGCGGTG 1353  
1307 AGCAGCACCGGAGACAGCATGACACTGTATGAGCTCCCGGAAAGGCCCAAGCGCATC 1366  
1354 ATCTGAGATATGAGTGCAGTACTATGAGAG--GAGCTCAGTGAATCAAGCCACA 1410  
1367 ATTCTGACATGAAATCAAGTACTCCAGAAAGGAGGAGGCTGAGGCTTGGCAAC 1426  
1411 GCAATAAAGCCCAACACAGGCTACG-----GGCTCAAAAGCGGCGCATCTAT 1464  
1427 ACTGTCAACAGCCAGAAAGACTCGGTGCGCTGAGCGGATGAAAGGCAATGCTCGTAC 1486  
1465 GTCTTCAGGTGGGCGGACGACCTGTGGACGCTTACGCGGCGCTACAGCGGCAAGATGAC 1524  
1487 ATGGTGAGGTCCGGCGCGCCACAGTGGTGAATACGCGCGTACAGCTCCCAACGAG 1546  
1525 TTCCAGACATGACAGAGCGGATACCAACAAGCATCCAGAGAAAGTTGCCATCATC 1584  
1547 TTTCAGACGACTGCGAGATGGCTCCACAGCAAGACTTCCAGAGAGCTTCTCATC 1606  
1585 ATCGGCTCTCGGCGCGCTGAGCTGTCTCTCATTTGCTGTGATCGCATCGT 1644  
1607 GTGGGTTCAGCCACCGGGGAGCTGCTGTGTGATCGTGGTGTGATCATCGTATTTGTC 1666  
1645 TGTACAGAGCGGGGTT-----TGAGCGTGTGACTCGAGTACAGCAAGCTGCAA 1698  
1667 TGTCTGAGAAAGGATGTACTGAAACAACCTCTGCTGCTGCTGGGAGGAGGAG 1726  
1699 CACTACACGAGTGGCCACA-----TAACCCAGGATG 1731  
1727 CGAACAGCACAGATCCCGAGTACACAGAGACCTGCAGCAATATGCTCTGGGATG 1786  
1732 AAGATCTACATCAATCCTTTCACCTACGAGAGCCCAACAGGACGAGCGGAGTTTGGC 1791  
1787 AAGTGTACATGATGCCCTTACCTTACCTATGAAAGCCCAATACATGCTGCGGAAATCGC 1846  
1792 AAGGAATGACATCTCTGTGTCAAAATTTGACAGGCTGATCGAGAGGAGGAGTTTGGC 1851  
1847 AAGAGATTTGATATCTCTGTGTCAAAATTTGAGAGGCTGATTTGAGAGGAGGTTTGGT 1906  
1852 GAGGTGTGAGTGGGCGACCGTGAAGCTGCGCAAGAGAGAGATCTTGTGGCATCAAG 1911  
1907 GAGGTGTGCGTGGGCGCTGAGAGTGGCTGGCGCGCTGAGATCTTGTGGCATCAAG 1966  
1912 ACCTCAAGTCTGGGCTACACGAGAGACAGCGCGGACTTCTGTGACGAGCTCCATC 1971  
1967 ACACTGAAGGTGGGCTACACAGAGAGGACAGCGCGGAACTTCTGTGATGGCCAGCATC 2026  
1972 ATGGGCGAGTTCACATCCCAACGCTATCCACTGTGAGAGGCTGTGAGCAAGAGCCG 2086  
2027 ATGGGCGAGTTCACACCCCAACATCATCCTGTGAGAGGCTGTGAGCAAGAGCCG 2086  
2032 CTTGTGATCATCATCAACCGATTCATGAGAAATGGCTCCCTGAGACTCTTCCGGCAA 2091  
2087 CTTGTATGATCATCATCAGAGATTCATGAGAACTGGGCTCTGCACTCTTCCCGGCTG 2146  
2092 AAGGATGGGAGTTTCAAGTCAATCAGCTGATCGAGTGGGAGTGGTGGGGCATCGAGCTGGC 2151  
2147 AATGATGGGAGTTTCAAGGTCATCCAGCTGATGGTGGGAGTGGTGGGAGCATCGCTGGC 2206  
2152 ATGAATTACTGGCAACATGATGATGTTTCAACCGTGAAGCTGGCTCCCGCAACATCTC 2211  
2207 ATGAATTACTTCAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2266  
2212 GTCAACAGCAACCTGTGTGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 2271  
2267 GTCAACAGCAACCTGTGTGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 2326  
2272 GATACCTCAGACCCCACTTACACACAGTGGCGGGGAAAGTTTCCCATCCGCTGGACA 2331

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Db 2327 GATCCAGCGCGACCCACCTACACAGCTCCCTGGGAGGCAAGATCCCATAGAGGTGGACA 2386
Qy 2332 GCCCGGAAAGCATCAGATACAGAGTTTACCTCGGAGCTGATGTTGGAGCTACAGC 2391
Db 2387 GCTCTGAGGCGATCGCTACCGCAATTCACTGCGGACGAGCTGTGGAGCTACAGC 2446
Qy 2392 ATGTGATGTTGGAGGTGATGCTTATGAGGAGGCGCCCTACTGGGACATGACCAACGAG 2451
Db 2447 ATGCTGATGTTGGAGGTGATGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2506
Qy 2452 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2511
Db 2507 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2566
Qy 2512 GCCCGGAAAGCATCAGATACAGAGTTTACCTCGGAGCTGATGTTGGAGCTACAGC 2571
Db 2567 GCACTGCAACGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2626
Qy 2572 GCCCAATGTTGCAACAGCGTACAGAGTATGATGATGATGATGATGATGATGATGATGATG 2631
Db 2637 GCACAGATTGTTCAACACGCTGACAGAGTATGATGATGATGATGATGATGATGATGATG 2686
Qy 2632 GCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2691
Db 2687 GCGAGCGTCCAGTCCGCTGCTCCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2746
Qy 2692 AGCTTTAAACAGTGTGAGAGTGTGAGAGGCAATCAAGATGATGATGATGATGATGATGATG 2751
Db 2747 ACCTTCAACACGCTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 2806
Qy 2752 TTGCGCAATGCGCGCTTACCTCTTTGAGCTGCTGCTCAAGATGATGATGATGATGATG 2811
Db 2807 TTGCTCAACAGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2866
Qy 2812 CTCGGGCTTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2871
Db 2867 CTAAAGATGAGTGTGAGAGTGTGAGAGGCAACAGAGATGATGATGATGATGATGATG 2926
Qy 2872 ATGCGGCGCGAGATGACCAAGATTCATGCTGTGAGGTTTGGC 2914
Db 2927 ATGAGGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2969

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APPLICATION NUMBER: JP 315806/1993
FILING DATE: 24-NOV-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4027 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: skeletal muscle myoblast
CELL LINE: L6
US-08-348-143-3

Query Match 51.5%; Score 1526.4; DB 1; Length 4027;
Best Local Similarity 71.4%; Pred. No. 0;
Matches 2083; Conservative 0; Mismatches 791; Indels 42; Gaps 4;

Qy 52 GAGCTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 111
Db 388 GAGCTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 447
Qy 112 AACATGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 171
Db 448 GCAATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
Qy 172 TGGCTTACGAGCAAGTTTATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
Db 508 TGGCTTACGAGCAAGTTTATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 567
Qy 232 TTTTTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 291
Db 568 TTTTTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627
Qy 292 AACCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 351
Db 628 AACCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687
Qy 352 GAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
Db 688 GAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 747
Qy 412 CTGGTGGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 471
Db 748 GCTGGGCGC-----GTTAAACCAAAAGTGCAGCTTGGGCGCTTTTCAAA 795
Qy 472 AGCGGCTTCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 531
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Qy 532 GTCTTCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
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Qy 652 GAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
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Qy 712 GCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
Db 1036 GGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1095
Qy 772 TGTCCATCTGGGACTTTCAAGGCCAAGGAGGATGAGGCTGTACCACTGTCCATC 831

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QY 1357 CTGGACTATGAGTGCAGTACTATGAAAGAGAGCTGATGAGTACACCCGACAGCCATA 1416  
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 Db 1696 TTGGACTATGAGTGAAGTATGTTGAAAGAGTAAAGCATGCGCTCCACTGTCCACAC 1755  
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 QY 1417 AAAAGCCCAACCAACAGGCGACAGGCGCTCAAAAGCGGCGCATATGCTTCCAGGTG 1476  
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 QY 1654 CGGGGTTTGAAGCTGTGACTGAGTACGAGACAGCTGCAACACTACACCAAGTGC 1713  
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 Db 1996 AAGCAGGCGCAGGCGCTGATGCAAGATACAGAGAAAGTTGACAGCAAT----- 2044  
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 QY 1774 GCAGTGGGAGTTTGGCAAGAAATTAATGACATCTCTGTCTCAAAATTTGAGCAGTATC 1833  
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 Db 2104 GCGCTCCGAGAGTTTGGCAAGAGATGATGTCTGCGCTCAAGATTCAGAGAGGTGAT 2163  
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 QY 1834 GAGAGAGGAGTTTGGCGAGTCTGCAAGTGCACCTGAAGTGCAGAGCAAGAGAG 1893  
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 QY 1894 ATCTTGTGSCATCAAGAGCTCAAGTCCGAGTACAGAGAGAGAGAGCCCGGAGCTTC 1953  
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 QY 2194 GCTGCGCGCAATCTCTGTCACAGAGCAAGCTGTGCAAGTGTGGAGTGTGGGCTG 2253  
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 Db 2524 GCTGCGCGCAATCTCTGTCACAGAGCAAGTGTGCAAGTGTGGAGTGTGGGCTG 2583  
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 QY 2254 TCAAGCTTTTGAAGAGAGTACTGAGAGCCCACTACAGCAATGCTGGGCGGAGAG 2313  
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 Db 2584 TCCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2643  
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 QY 2314 TTCCCATTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2373  
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 Db 2644 ATCCCTATTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2703  
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 QY 2374 GATGTGAGAGTACGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2433  
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 Db 2704 GATGTGAGAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2763  
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QY 2434 TGGAGATGACCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2493  
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 Db 2764 TGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2823  
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 Db 2824 CCATGAGTGGCGGAGCGCTGCAACAGTATGATGATGATGATGATGATGATGATGATGATG 2883  
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 Db 2884 AACCTAGGCGCAAGTGTCCCAATGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2943  
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 QY 2734 GGGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2793  
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 Db 3184 CTGACAGATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3243  
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 QY 2914 CATTACCTGCTCGGCTCACTCTCTCTCAAGAGC 2949  
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 Db 3244 CGCTCAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3279  
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RESULT 11  
 US-08-571-785-3  
 ; Sequence 3, Application US/08571785  
 ; Patent No. 5804411  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TAJIMA, HISAO  
 ; APPLICANT: KITAGAWA, KOICHIRO  
 ; APPLICANT: OHNO, HIROYUKI  
 ; APPLICANT: UENO, TOSHIO  
 ; TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140  
 ; TITLE OF INVENTION: and dnms encoding it  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS  
 ; STREET: 2100 Pennsylvania Avenue, N.W.  
 ; City: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20037-3202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/571,785  
 ; FILING DATE: 13-DEC-1995  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/348,143  
 ; FILING DATE: 23-NOV-1994  
 ; APPLICATION NUMBER: JP 315806/1993  
 ; FILING DATE: 24-NOV-1993  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)293-7060  
 ; TELEFAX: (202)293-7860



TELEX: 6491103  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4027 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: rat  
 TISSUE TYPE: skeletal muscle myoblast  
 CELL LINE: L6  
 US-08-571-785-3

Query Match 51.5%; Score 1526.4; DB 1; Length 4027;  
 Best Local Similarity 71.4%; Pred. No. 0;

Matches 2083; Conservative 0; Mismatches 791; Indels 42; Gaps 4;

QY 52 GAGCTGGCGTGGATGGTGCATCTCCATCAAGGTGGAGAGGTAGTGGCTACGATGAG 111  
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 QY 112 AACATGAAACGATCCGCAAGTACAGGTGTGCAGGTGTTGAGTCAGCAAGCCAGAACAC 171  
 Db 448 GGCATGATCTTCCGCAAGTATCAGGTGTGTACGTGCGGAGTCCAGCCAGAACAC 507  
 QY 172 TGGCTACGAGCAAGTTTATCCGGCGCGTGGGGCCACCGCATCCAGTGGAGATGAAG 231  
 Db 508 TGGCTACGAGCAAGTTTATCCGGCGCGTGGGGCCACCGCATCCAGTGGAGATGAAG 567  
 QY 232 TTTTCGCGTACGATCGAGCAAGTACCCAGCGTGGCGTCCCTGCGCAAGAGACCTTC 291  
 Db 568 TTTACGCTGAGAGATTGCAACAGCATCCCAACATCCCTGCGTCCGCAAGAGACCTTC 627  
 QY 292 AACCTTATTACTANGAGCGCTGACTTGTGACTGCGCCACCAAGACCTTCCCAACTGATG 351  
 Db 628 AACCTTATTACTANGAGCGCTGACTTGTGACTGCGCCACCAAGACCTTCCCAACTGATG 687  
 QY 352 GAGAAATCCATGGGTGAGAGGTATGATCCATTCAGACCGAGAGAGCTTCCAGAGTGAAC 411  
 Db 688 GAGAAATCCATGGGTGAGAGGTATGATCCATTCAGACCGAGAGAGCTTCCAGAGTGAAC 747  
 QY 412 CTGGGTGGCGCGGTATGAAATCAACACCGAGGTGCGGAGCTTGGAGACTGTGCGCGC 471  
 Db 748 GCTGGGCGC-----GTTAAACAACAAAGTGGCGAGCTTGGGCGCTTTCCAA 795  
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 Db 796 GCGGCTCTACCTGCGCTTCAGAGATATGCGCGCTGCATGTCCCTCATCGCGCTGCGT 855  
 QY 532 GTCTTCTACCGCAAGTGGCCCGCCGATCATCCAGAAATGGCGCATGTTCCAGAGAAACCTG 591  
 Db 856 GCGTCTCTACCGCAAGTGGCCCGCCGATCATCCAGAAATGGCGCATGTTCCAGAGAAACCTG 915  
 QY 592 TCGGGGGTGAAGAGACATCGCTGGTGGCTCCCGGGGCACTGCATCGCCAAATGCGGAA 651  
 Db 916 ACGGGGGTGAAGAGACATCGCTGGTGGCTCCCGGGGCACTGCATCGCCAAATGCGGAA 975  
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 Db 1216 GCAGACTGAGCCCTCGGATGCTGCTGACACACATCTCCCTCGCGCCAGGCTGAG 1275  
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 Db 1276 ATTTCAGTGTCAATGAGACCTCCCTCATGCTGAGTGGAGCCCTCCCGGACTCCGA 1335  
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 Db 1336 GGCAGAGAGAGACCTGCTTACAAATCATCTGCAAGACT-----GTGGC 1395  
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 Db 1396 GCGAGTCCGGGCACTGTTTACAGCGTGTGATGACAAAGTGGAGTTGAGGCCCGGACGCTG 1455  
 QY 1117 GGCCTGACCGGACCGGATTTACATGATGACCTGCTGGCCCAACCGCACTACACCTTC 1176  
 Db 1456 GGCCTGACCGGACCGGATTTACATGATGACCTGCTGGCCCAACCGCACTACACCTTC 1515  
 QY 1177 GAGATCAAGGCTGTGAAAGGGGTTACTGACAGAGCCCTTCTGCGTCAAGTTGCGCT 1236  
 Db 1516 GAGATCAAGGCTGTGAAAGGGGTTACTGACAGAGCCCTTCTGCGTCAAGTTGCGCT 1575  
 QY 1237 GTGAATCAGCAGCAGCAACAGGAGCTTCATGCGAGTGTTCATCATCATCAGTGAAC 1396  
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 Db 1756 CAGAAAGAACTGTGTAACAGTGTGAGAGAGAGCTCAGCGGCGGCTATGAGTTCAGGTG 1815  
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 Db 2224 GTTTCGTGGCATGAAGAGCTCAAGTGGGATACAGCGAGAGGAGCAGCGGAGATTC 2283

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QY 1954 CTGAGGAGCCCTCATCATGAGGCGAGTTCGACCATCCCAAGCTATCCACCTGAGAGGT 2013
DB 2284 CTGAGTGAAGGCTTCATCATGAGGCTCAATTTGACATCCAAATATATATACGCTAGAGGGC 2343
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DB 2524 GCTGCGCGCAACATCTGCTCAACAGTTCATGAGTGAAGTTCATGAGTGAAGTTCAGTCCGCTG 2583
QY 2254 TCACGCTTTCTAGAGAGATACCTAGACCCCACTACACCAAGTGGCTGGGCGGAAG 2313
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DB 2644 ATCCCTATCCGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2703
QY 2374 GATGTGGAGAGTCAAGGATGTGATGTGGAGAGTGTGATGTGATGTGATGTGATGTGATGTG 2433
DB 2704 GATGTGGAGAGTCAAGGATGTGATGTGGAGAGTGTGATGTGATGTGATGTGATGTGATGTG 2763
QY 2434 TGGAGATGACCAACAGAGATGATATGATGATGATGATGATGATGATGATGATGATGATG 2493
DB 2764 TGGAGATGACCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2823
QY 2494 CCCATGAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2553
DB 2824 CCCATGAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2883
QY 2554 AACCAACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2613
DB 2884 AACCTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2943
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RESULT 12  
US-08-571-785-4  
; Sequence 4, Application US/08571785

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; Patent No. 5804411
; GENERAL INFORMATION:
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAJIMA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
; TITLE OF INVENTION: A No. 5804411el polypeptide of protein p140
; TITLE OF INVENTION: and DNAs encoding it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEA & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/571,785
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 4.35
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/348,143
; FILING DATE: 23-NOV-1994
; APPLICATION NUMBER: JP 315806/1993
; FILING DATE: 24-NOV-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4027 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: skeletal muscle myoblast
; CELL LINE: L6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 262..3243
; IDENTIFICATION METHOD: by similarity to some other pattern
; US-08-571-785-4

Query Match 51.5%; Score 1526.4; DB 1; Length 4027;
Best Local Similarity 71.4%; Pred. No. 0;
Matches 2083; Conservative 0; Mismatches 791; Indels 42; Gaps 4;

QY 52 GAGGTGGGCTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 111
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DB 448 GCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
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DB 508 TGGCTAGGAGACCAATTTATCCGCGCGCGTGGGGCCACCGCATCCACAGTGAAGTGAAG 567
QY 232 TTTTCGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 291
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Oy 412 CTGGGTGGCCGCGTCATGAAATCAACACCGAGGTGGAGGCTTGGAGCTGTGTCCGC 471
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Oy 592 TCGGGGCTGAGAGCATCGCTGTGGCTGCCGCGGCGAGCTGCATGCGCAATGCGGAA 651
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Oy 712 GGGGCTCATGTGCAAAAGCAGCTTTCGAGGCGCTTGAAGATGGCAGCCCTTCGCGAGGT 771
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Oy 952 AATTTCAGTGTCAATGAGACCTCTCATGTGTGAGTGGACCCCTCCCGGCACTCCGGA 1011
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Db 1396 GGAGGTCCGGGCACTGTTACAGCTGTGATGACAAAGTGTGAGTTCAGGCGCCGACAGCTG 1455
Oy 1117 GGCCTGACCGACCAAGCATTTATACATCACTGTGACCTGTGGCCACACCAAGTACACCTTC 1176
Db 1456 GGCCTGACCGACAGCGCGGCTCCACATCAAGCAGCTGTTGGCCACACCGGCTACACCTTT 1515
Oy 1177 GAGATTCAGGCTGTGAAGCGGCTTACTGACAGAGCCCTTCTCGGCTAGTTCGCTCT 1236
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Oy 1357 CTGGACTATGAGCTGCAGTACTATGAAAGGAGCTCAGTGTACAAAGCCACAGGCATA 1416
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Db 1636 TTGACATATGAGATGAAGTACTTTTGAAGAGTAAAGGATCGCTCCACTGTACACAGC 1755
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Db 1876 AGTGAAGAGGCTCAGGGGCGCCAGCAGCTTCAAGAGCAGCTTCCCTAATTTGTGGATTC 1935
Oy 1594 TCGGCGCTGTGGCTGTCTTCTCATTTGCTGTGTATGATGCGCATCGTGTATACAGA 1653
Db 1936 ACCGTAGCGGTGTGTGTATGTGGTGGTGTGTGTGTATGTGTGTGTGTGTGTGTGTGT 1995
Oy 1654 CGGGGTTTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1713
Db 1996 AAGCAGCGCCAGGCGCTGTATGACAGAAATACAGGAAAGTTGCACCAAT----- 2044
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Db 2224 GTGTGTGTGGCATCAAGCACTGTGAAGTGTGATTCACGAGAGAGGAGGCGGAGCTTC 2283
Oy 1954 CTGACGGAAGCTCTCATCATATGGCGCAGTTGACATCCCAAGCTACCTCAGGTGAGGT 2013
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Oy 2014 GTCTGTACCAAGACACACCTGTGATGATCATACCGAGTTATGGAATATGCTCCCTG 2073
Db 2344 GTGTGTACCAAAAGTGTGCTACAGTGTATGTCTGAGTGTATGAGAACTGTGCGCTG 2403
Oy 2074 GACTCTTTCGCGCAAAAGATGAGTGTGACAGTGTATGATGATGATGATGATGATGAT 2133
Db 2404 GACTCTTTCGCTACGGCTCATATGACGGGAGTTTACAGTATCATGCTTGTGGCATGTG 2463
Oy 2134 CGGGCATCTGCAAGCTGTGCAATGAAGTACCTGTGAGACATGAACATATGTTACCGTACCTG 2193
Db 2464 CGTGGCATGTGTGCGCGGATGAAGTACTGTGTGAGATGAACGTGACGCTGACCTG 2523
Oy 2194 GCTGCGCGCAACATCTGCTCAACAGCAACCTGTGTGTGCAAGTGTGCGGACTTTGGGCT 2253
Db 2524 GCTGCGCGCAACATCTTGTCAACAGTAACTGTGTGTGCAAGTGTGCACTTTGGGCT 2583
Oy 2254 TCACGCTTCTGAGAGCATATCTGACAGCCACCTACACAGTGTGCTTGGGCGGAAG 2313
Db 2584 TCACGCTTCTGAGAGCATATCTGACAGCCACCTACACAGTGTGCTTGGGCGGAAG 2643
Oy 2314 TTCCTCATCCGTGAGCAGCCGCGGAGGATCAAGTATGAGTATGAGTATGAGTATGAGTAT 2373
Db 2644 ATCCGATATCGTTGAGCAGCCCGCAGAGGCGCATATGAGTATGAGTATGAGTATGAGTAT 2703
Oy 2374 GATGTGTGAGCTACGGCATTTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2433
Db 2704 GATGTGTGAGCTACGGGATGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2763
Oy 2434 TGGGACATGACCAAGAGTATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2493
Db 2764 TGGGACATGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2823
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QY	2494	CCCATGACATGCCCCGACGCGCCCTGCGACACAACTATCTGAGCTGTTGGCAGAAAGACCG	2553
Db	2824	CCCATGAGCTGCCAGCGGGGGCTGACACAGCTATCTGAGCTGTTGGGTGGGGACCG	2883
QY	2554	AACCACGGCCCCAAGTTCGGCCAAATTTGTCAACGCGTATGACAGATGATCGCAATCC	2613
Db	2884	AACCTCAGGGCCCAAGTTCCTCCCAAAATGTCACACGCTGTAGACAACTTATCGCAATCT	2943
QY	2614	AACAGCCCTAAAGCCANTGGGGGCCCTCTGCTGGAGTAACTGTCGCTGTSAGCCG	2673
Db	2944	GCCAGCCTCAAGGTCATCGCCAGTGCCTCCCATCTGGGTATGTCCACATCCCTCTTAACCGC	3003
QY	2674	ACGATCCCCGACATACACACACTTTAAACACGGTGGAGAGATGGCTGGAGCCATCAAGTG	2733
Db	3004	ACGGTCCCATGATTATACGACTTCACAGACGGTGGGAGATGGCTAGATGCCATCAAGATG	3063
QY	2734	GGGCAGTACACAGAGAGCTTCGCCAAATGCCCGCTTCACTCTTTGACAGCTGTGTTAG	2793
Db	3064	GGGGGGTATAAAGAGACTTCGTGGGTGGGGTTTTGGCTCTCTTAGACTGTGTGGCCAG	3123
QY	2794	ATGATGATGAGAGGACATTTCTCCGGGTGGGGGTACATTTGGCTGGGCACACAGAAAAATC	2853
Db	3124	ATGAGCTCAGAAAGATCTGCTTAAGAGATCGGGGTCACTTTGGCCGGCCACCAGAAAGATC	3183
QY	2854	CTGAACAGTATCCAGGTGATGGGGCGCAGATGAACCAAGTTCAGTCTGTGGAGTTTGA	2913
Db	3184	CTCAGCGATATCCAGGACATGCGGGCTGCAGATGAACACAACTCCCGTCAAGGTCTGA	3243
QY	2914	CATTCACTGTGGGTGTACACTTTCCGCAAGCC	2949
Db	3244	CGCTACGCTCACGCAAGGGGCTGGGCCCCCGGGAC	3279

RESULT 13  
 US-08-348-143-2  
 Sequence 2, Application US/08348143  
 Patent No. 5506205  
 GENERAL INFORMATION:  
 APPLICANT: TAJIMA, HISAO  
 APPLICANT: KITAGAWA, KOICHIRO  
 APPLICANT: OHNO, HIROYUKI  
 APPLICANT: UENO, TOSHIO  
 TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs  
 TITLE OF INVENTION: encoding it  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20037-3202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348,143  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 315806/1993  
 FILING DATE: 24-NOV-1993  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)293-7060  
 TELEFAX: (202)293-7860  
 TELEX: 6491103  
 INFORMATION FOR SEQ. ID NO.: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2982 base pairs  
 type: nucleic acid

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? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? ORIGINAL SOURCE:
? ORGANISM: rat
? TISSUE TYPE: skeletal muscle myoblast
? CELL LINE: L6
US-08-348-143-2

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Query Match	51.3%;	Score 1520.8;	DB 1;	length 2982;
Best Local Similarity	71.7%;	Pred. No. 0;		
Matches 2066;	Conservative 0;	Mismatches 772;	Indels 42;	Gaps 4;

QY	52	GAGCTGGGGTGGAGTGGATGCACTCCATCAACGGGTGGGAAGAGGTGGATGGTCAACGTGAG	111
Db	127	GAGCTGGCATGGAACTCATCTCATCCAGAGAGTGGGGTGGGAAGAAAGTGGAGCCCTACATGTA	186
QY	112	AACATGAACAGATTCGGCAGCTACAGAGTGTGCAACGTGTTTAGTCMAAGCCAGAAACAC	171
Db	187	GCCATGAGATCCTTAATCCCGACAGTCAAGGTGTGTAAAGTGGGCGAAGTCCAGAGAAACAC	246
QY	172	TGGCTAGAGAACAAATTATCCGGCGCGGGGGGCCACCGCATCCACGTGGAGATGAAG	231
Db	247	TGGCTGGGGAACCGGTTTCACTGTGGCGGGGAAGTCCAGGCGCTCTACGTGGAGCTGAAG	306
QY	232	TTTTGCGTGGTGAATTCACAGACATATCCACGCTGCTGTGCTCTGCAAGGAGACCTTC	291
Db	307	TTTTACCGTAGAGATTGGCAACAGCATATCCCAATCCCTGGCTCCGCAAGGAAACCTTC	366
QY	292	AACCTATATTAATATGAGGGCTGATCTTGAATGGGCAACAAAGACCTTCCCAACATGGATG	351
Db	367	AACCTTTTTTACTACAGAGCTGTATAGCGATGTGGCTCAACCTCTCTCTCTTTGTGGATG	426
QY	352	GAGAATCCATAGGCTGAAGTGGATACCATTTGCACGCCAGAGAGCTTCCAGAGGTGAC	411
Db	427	GAGAAACCCCTACGTAAGAAAGTGAGACACCATTTGCCAGATAGAGAGCTTCTGGCGGTGAC	486
QY	412	CTGGGTGGCGCGCTCATGAAATCAACACCCGAGGTGCGGAGCTTGGAGACTGTGTCCGC	471
Db	487	GCTGGGGGCG-----GTTAACACCAAAAGTGGAGCTTGGGCGGCTTTCACAA	534
QY	472	AGCGGCTTACCTGAGGCTTCCAGAGCATGAGGGGTGGATGTCCTTCATTCGCGTGCCT	531
Db	535	GCGGCGCTTACTTGGCTTCCAGAGACAGAGGTGCTGATGTCAATCATCTCTGTGGCC	594
QY	532	GTCCTTACCGCAATGGCCCCGCGCATATCCAGAAATGGCGCATCTTCCAGGAAACCTG	591
Db	595	GCCCTTACAAAGAACTGTGCATCCACACATGCGAGGCTTGCACTTCCCGAGAGCCCTC	654
QY	592	TGCGGGGCTAGAGACATGCTGGTGGGCTGCCCGGGGAGCTGCATGCCAATCGGAA	651
Db	655	ACGGGGGCTAGCGCACTTGGCTGGTATTTGCCCTGGGCACTGCATCCCTAAACGTGG	714
QY	652	GAGTGGATTTACCATCAAGCTCTACTGTAAACGGGGAGCGGAGTGGTGGTGCATC	711
Db	715	GAGTGTCTGTACCGCTCAAGCTCTACTGGAATGGGAGGAGGGGAATGGATGGTGCCTT	774
QY	712	GGGCGCTGCATGTGCAAGAGAGGCTTCCAGAGCGCGTTGAAATATGGCAACGCTGTGCGGAG	771
Db	775	GGGGCGCTCAACCTGCGCTACTATGGCCATGAGCCAGCGCGCAAGAGACCCAGTGGCGCGC	834
QY	772	TGTTCATCTGGAGCTTCAAGGGCCACCAAGGGAGTGAAGGCTGTAAACCATGTGCCATC	831
Db	835	TGTTCCTCCCTGGAGCTACAAAGGCAAGGCAAGGAGAGGGGCGCTGCTCCCTGTCCCCC	894
QY	832	AACAGCCGAGCACTTCTGAAGGGGCGCACCACTGTGTCTGGCGCAATGGCTACTACAGA	891
Db	895	AATAGCGGCAACACTTGGCGGCTGCAGACATGTGCACTGTCACAATTAATTTCTACGCG	954
QY	892	GCAGACTGGACCCCTGGACATGCGCTTGACACACATCCCTCGCGGCCACAGGCTGTG	951
Db	955	GCGAGCTACACACACGCGGACACGCGCTACACAGGTGCGCTGTCTCCCGCGGGGTGTG	1014

Oy	952	ATTCACAGTGCATGAGACTCCCTCCTCAAGCGTGGAAATGGAGACCCTCCCGGACCTCCGA	1011
Db	1015	ATTCTCATGTGAATYGAGACTCGCTGATCTCTGATGGAGTGAGGCCCGGACCTTTGGC	1074
Oy	1012	GCCGAGAGGACCTCGCTCAACATCATCTGCCAAGCT-----GTGGC	1056
Db	1075	GAGAGAGATGACCTCTTTTAATAATGTTATCTGTAAABAATGGCGGTGGACGCTGGGGCT	1134
Oy	1057	TGCGGCGGGGGTGCCTTCACCCGCTCGGGGACAATGTACAGTAGCACACACGACGTA	1118
Db	1135	GGAGGTCGCGGACCTCTGTACCGCTGTGATGACAAAGTGAGATTGGAGCCCCGACAGCTG	1194
Oy	1117	GGCGTACCGGACGACGATTTACATCAGTAGCCTCTGGGCCAACACCGATGACACCTTC	1176
Db	1195	GGCTTGACCGAGCGCCGGGTCCACATATAGCACCTTGTGGCCACACCCGCTACACCTTT	1254
Oy	1177	GAGATCCAGGCTGTGAACGGCGTTACTGTGACACAGCGCCCTTCTCGCTCAGTTCCCTCT	1238
Db	1255	GAGGTGACGGCTGTCAACGGCGCTCTCGGAAAAGGCCTTTGGCGGCCCGCGATATGACCT	1314
Oy	1237	GTGAACATCACACACCAACGAGGACGCTCCATCGGACGTCCATCATCATGATAGGTAGC	1296
Db	1315	GTGAATATCACACCAACCGAGCGCCGCCCTCAAGAAGTCTCATCGCTCAGTTCATCGACAGC	1374
Oy	1297	CGCACCGGAGACCATTTACCCTGTGTGGTGTCCACCGGACACGACCAATGGCGTGTAC	1356
Db	1375	AGTTTACAGGAGACACCTTCGACCTGTCTGTGGGACACCCC CGGAGCGGCTTACGGAATCTAC	1433
Oy	1357	CTGGACTATGAGCTGACGTACTATGAAAGAGAGCTCAGTAGATACAAACCCACACCATTA	1416
Db	1435	TTGGACTATGATGATGAGTAGTACTTTGAAAGAAGTAAGAGCATGGCTCCACTGTACACAGC	1494
Oy	1417	AAAACCCCACCAACACGGTACAGGGGCTTCAAAGCCGGGCGCATATGTCTTCCAAGTG	1478
Db	1495	CAGAAGAACTCTGTACAACGTGAGACGTGACACCCGACCCCGCGCTATGTACTTGAAGTTC	1554
Oy	1477	CGGCGACGACACTGTGGGAGAGCTACGGGCGCTACAGCGGCAAGATGACTTCCAGACATGT	1538
Db	1555	CGGGCTGCAACAGTAGAGAGGTTACGACAGTATAAGCCGCCACAGCTAGTTTTAGACACAG	1614
Oy	1537	ACAGAAAGCCAGTACACAGAC--AAGCATTCAGAGAAAGTTGCCACTCATCTGCGGCTCC	1593
Db	1615	AGTGAAGAGAGCTCAGGGGCGCCACAGACCTTCAAGACACACTTCCCTTAATTTGTGGAGATC	1674
Oy	1594	TGCGCCGCTGGCCGTGGCTTCTTCATTTGCTGTGTGTATCGCCATCGTGTGTAAACAGA	1655
Db	1675	ACCGTACTGTGCTTTGTCTTTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1734
Oy	1654	CGGGGGTTTGAGCGTGTGTGACTCGGAGTAGACGAGCAACCTGCACACACTACACAGTGGC	1713
Db	1735	AAGCAGCGCCAGGGGCTGTATGCAAGATACACGAGABAAATTTGCAAGAT-----	1788
Oy	1714	CACATTAACCCAGGACATGAAGATCTACATCGATCTTTTACCTACGAGAGACCCCAACAG	1773
Db	1784	-ACGTGTGCCCCCAGAGTAAGAAAGTTTAACTATGACCCCTTAACGACGAGATCCCAATGAG	1842
Oy	1774	GCATGTGGGAGTTTGGCCAAAGGAATTTGACATCTCTGTGTCAAAATTGAGCAGGTGATC	1833
Db	1843	GCGCTCGAGAGTTCGCGCAAGGAGATTCGATGTCTCTGGGTCAAGATTCAGAGAGGTGATTT	1902
Oy	1834	GGACAGAGGAGTTTGGCGAGGTCTGACAGTGGCGACCTCAACGTGCGACCAAGAGAAAG	1893
Db	1903	GGAGCTGGGAGATTTGGGGAAGTGTGCGGGGCTGGGCTTAAACTGCCCCGCGCGGGAG	1963
Oy	1894	ATCTTTTGTGGCATCAAGACGCTCAAGTGGGGCTTACACGGAGACAGCGCGGAGCTTTC	1953
Db	1963	GTGTCTTGTCGCGCATCAAGACACTGAAGTGTGGATACACGGAAGGACAGCGCGGAGCTTTC	2022
Oy	1954	CTGAGCGAAAGCTTCCATCATGTGGGCGCAGTTTCGACATCCCAAGGTCACTCAGCTGGAAGGT	2013
Db	2023	CTGAGTAGGCTTCCATCATGTGGGTCAATTTGACACATCCAAATATATCTCGTTAGAGGGC	2082

0Y	2014	GTGGGACCAAGACACACCTGGTAGATCATACCGAATTCATGTGGAAGAAAGGCTCCCTG	2073
0Y	2014		
Db	2083	GTGGTCACCAAAATCGTCCAGTCATGATCTCTACGATTTATGGAAGAACTGTGCCCTG	2142
0Y	2074	GACTTCCTTTCCCGGCAAAAAGATGGGGAGTTTCACAGTATCATCCAGTCGGTGGCATCTGCT	2133
Db	2143		
0Y	2134	CGGGGCATCGCAGCTGGCATGAAGTACCTGGCGACAGATGAACTATGTTTCAACCGTGACCTG	2193
Db	2203	CGTGGCATTTGCTGGCGGGCATGAAGATCTTGTCTGAATGATGAACGTACGTGCACCGTCACTC	2262
0Y	2194	GCTGCGCGCAACATCTCTCTGTCAACAGCAACCTGTGTCAAGGTGTCCGACTTTGGGCTC	2253
Db	2263	GCTGCGCGCAACATCTCTGTCAACAGTAACTTGGTCTGCAAAAGTATCTGACTTTGGGCTC	2322
0Y	2254	TCACGCTTTTGAAGGAGCAATACCTCAGACCCCACTACACCAAGTACGCTGGGCGGAAG	2313
Db	2323	TCGCCCTTCTCGTGGAGAGACAGACCCCTCAGACCCCACTACACCAAGTACGCTGGGCGGAAG	2382
0Y	2314	TTCCCATCCGCTGGAGACGCCCGGGAAGCCATCAGTACCGGAAGTTCACTCTCGGCACT	2373
Db	2383	ATCCCTATTCGCTGGAGACCGCCCAAGAGGCCATGACTATGCGAAGTTCACTGCTCGACG	2442
0Y	2374	GATGTGTGGAGACTACGGCATTTGTCTATGTGGAGAGTATGTCTCTATTTGGGAGAGCGGCTTAC	2433
Db	2443	GATGTGTGGAGACTACGGGATTCGTCTATGTGGAGAGTATGAGTTAGGGAAGGAGACCAATAC	2502
0Y	2434	TGGGACATGACCAACAGAGTATATCAATAGCCATTGACAGAGACTATCGCTGGCCACCG	2493
Db	2503	TGGGACATGAGACCAACAGAGTATATCAATAGCCGTATGACCGGTAGACAGACATATCGGTTACCAACC	2562
0Y	2494	CCCATGGACTGCCCCGAGCGCCCTTGACCAACATCATGCTGGAGTGTGGCAGAAAGACCGC	2553
Db	2563	CCCATGGACTGCCCCAGCGCGGCTTGACCAACATCATGCTGGAGTGTGGGTTGGGCGGAGCCGG	2622
0Y	2554	AACCAACGGGCCCAAGTTCTGGCCAAATTTGTATACACGCTTAGACAAATGATATCCGCAATCCC	2613
Db	2623	AACCTCAGGGCCCAAGTTCTCCCAAAATCTGTACACACCTTAGACAAAGTTATTCGGCAATCT	2682
0Y	2614	AACAGCCTCAAAAGCCATGGGCGCCCTCTCTCTGGGATCAACCTGGCGCTGCTGGAGACCG	2673
Db	2683	GCCAGCCTCAAAAGTCAATGGCCAGTGCCTCCCTCTGGCATGTCCGAGCCCTCTTAGACCGC	2742
0Y	2674	ACGATCCCCGCACTACACACGCTTTTAACACGCTGAGAGATGCGCTGGAGGCCATCAAGATG	2733
Db	2743	ACGATCCCCAAGTTATAGACGCTTTCACGACGCTGGGAGCATGGCTAGATGCCATCAAGATG	2802
0Y	2734	GGGCAGTACAAGGAGAGCTTGGCCAAATGCGCGCTTCACTCTTTGACGCTGCTGTCTAG	2793
Db	2803	GGGAGGTATTAAGAGAGACTTGTGTGGTGGCGGGTTTGGCTCTTTGACCTGTGTGGCCGAG	2862
0Y	2794	ATGATGATGGAGAGCATTTCTCCGGGTTGGGGTCACTTTGGCTGGCCACCAAGAAAATATC	2853
Db	2863	ATGATGTCGAAGAATCTGTCTTAAGAGATCGGGGTCACTTTGGCCGCGCACCAAGAAAGATC	2922
0Y	2854	CTGAACAGTATTCAGGTGATGCGGGCGGCACATGAACAGCAATTCAGTCTGTGGAGTTTGA	2913
Db	2923	CTCAGCACTATTCAGGACATGCGGCTGCAATGAACCAACACACTGCCGCTGCAGGTTCTGA	2982
RESULT 14			
; Sequence 2, Application US/08571785			
; Patent No. 5804411			
; GENERAL INFORMATION:			
; APPLICANT: TAJIMA, HISAO			
; APPLICANT: KITAGAWA, KOICHIRO			
; APPLICANT: OHNO, HIROYUKI			
; APPLICANT: UENO, TOSHIO			
; TITLE OF INVENTION: A No. 5804411el Polypeptide of Protein p140			
; TITLE OF INVENTION: and Dnas encoding it			
; NUMBER OF SEQUENCES: 16			

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RESULT 14
US-08-571-785-2
; Sequence 2, Application US/08571785
; Patent No. 580411
;
; GENERAL INFORMATION:
;
; APPLICANT: TAJIMA, HISAO
; APPLICANT: KITAGAWA, KOICHIRO
; APPLICANT: OHNO, HIROYUKI
; APPLICANT: UENO, TOSHIO
;
; TITLE OF INVENTION: A No. 580411a1 Polypeptide of Protein p140
;
; TITLE OF INVENTION: and Dnas encoding it
;
; NUMBER OF SEQUENCES: 16

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CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/571,785  
FILING DATE: 13-DEC-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/348,143  
FILING DATE: 23-NOV-1994  
APPLICATION NUMBER: JP 315806/1993  
FILING DATE: 24-NOV-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2982 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: skeletal muscle myoblast  
CELL LINE: L6

OY	2674	ACGATCCCGACCTACACACACCTTTAAACAGCGTGTGAGAGATGGCTGGAGCCATCAAAAGT	2733
Db	2743	ACGGTCCCAAGTTATTACGACCTTCACAGACCGTGTGGGCACTGGCTGAAATGCCATCAAGATG	2802
OY	2734	GGCAGATTCACAAGAGAGACCTTCCGCAATGCCGGCTTCACCTCTTTGAGCTCGTGTAG	2793
Db	2803	GGGAGGTATAAAGAGACCTTCGTGCGTGGCGGGTTTGGCTCTTTGACCTGGTGGCCAG	2862
OY	2794	ATGATGATGGAGGACATTTCTCCGGGTTGGGGGTACCTTTGGCTGGCCACCAGAAAAAATC	2853
Db	2863	ATGACTCCAGAAGTTCGTCTAAAGAAATCGGGGGTCACTTTGGCCGGCACACAGAAGAAATC	2922
OY	2854	CTGAACAGTATCCAGGTGATCGGGCGCAGATGAACACAACTTCACTCTGTGGAGGTTTGA	2913
Db	2923	CTCAGCAGTATCCAGGACATGGCGGCTGCAGATGAACACAACTCCCGGTGAGGTTCTGA	2982

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RESULT 15
US-08-162-809-1
; Sequence 1, Application US/08162809
; Patent No. 5457048
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162, 809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3133 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(3..419, 421..2858)
US-08-162-809-1

Query Match 49.6%; Score 1469.6; DB 1; Length 3133;
Best Local Similarity 70.7%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 704; Indels 164; Gaps

0Y 18 AGAAGCGCTAAATGAGCTCCACATACAGCGACGCTGAGCTGGGCTGGATGCTGCATCTCC 77
Db 2 AGAAACCTGATGAGACACAGCAGCAGCGACGCTGAGCTGAGCTGGGCTGAGCTCCAAACCTCC 61
0Y 78 ATCAGGCTGGGAGAGAGGTGAGTGGCTACGANTGAGAAATGAAACAGAGATCCGACGTACCA 137
Db 62 GTCAAGGTGGGGAAGAGTGAAGTGGCTACGACGAGAACTGAGACACATCCGTACCTACCA 121

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138 GGTGTCACAGTGTGTGATGACAGCAGCAACACTGCTACGGACCAAGTTATTCGGCG 197  
122 GGTGTGACAGTGTGTGACAGCAACCAACAACTGCTCTTCAACCTTCAACCG 181  
198 CCGTGGGGCCACCGACCTGAGATGAAGTTTGGTGGCTGCTGACAGCAAT 257  
182 GCCCGAGCCGACCGATCTACAGTGAAGTGCCTTACCTGCTGGGACTGCGACGCT 241  
258 CCCAGGCTGCTGGCTGCTGCAAGAGACCTTCAACCTTATTTAGAGGCTGCT 317  
242 CCCAGAGTCCCGGCTGCTGCAAGAGACCTTCAACCTTATTTAGAGAGACGCTC 301  
318 TGACGTGCGCCACCAAGACTTCCCACTGATGAGATTCATGGGTGAAGTGGATAC 377  
302 TGTGATGCTGCTGAGAGAGTGGCTTGTGAGGAGGACCCCTTACCTCAAGTGGAC 361  
378 CATTTGACGCGAGAGAGCTTCTCCAGTGGAGCTGGTGGCGGCTCATGAAGATCAA 437  
362 CATTTGCTGAGAGAGCTTCTCCAGTGGAGCTTGGTGGAGCTTGAAGATGA----- 415  
438 CACGAGGTGGAGAGCTTGGAGCTTGTCCGACGCGCTTCTACCTGGCTTTCAGGA 497  
416 ----- 415  
498 CTATGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 557  
416 -----GGTCTTCTCAAGAGTGGCCAGCGT 443  
558 CATTCAGAAATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617  
444 GGTGACAGACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503  
618 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677  
504 GACAGCAGCGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563  
678 CTGTAAGCGGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737  
564 CTGCAAGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 623  
738 CGAGGCGCTTGAAGATGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797  
624 TGAGCC---GGAAAAACAAGTGGCTTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 680  
798 CCAAGGAGTGAAGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857  
681 TCAGGCTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740  
858 CACCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 917  
741 ACCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800  
918 CTGCAACACCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977  
801 CTGCAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860  
978 CATGCTGAGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1037  
861 CATCTGAGTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920  
1038 CATCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097  
921 TGTCTGAGAAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980  
1098 GTACGACACCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1157  
981 GTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040  
1158 CGACACCGCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217  
1041 ACACACCGCTTACCTTGTGAGATTCAGGCGGTCAACGGGCTTTCACACAGAGCCCTT 1100

1218 CTCGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1277  
1101 CCCACCCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160  
1278 CATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1337  
1161 CATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1220  
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